Sequence:

Run on:

Searched:

Database

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AJ243888 Arabidops
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AJ010500 Arabidops
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AC112592 Rattus no
Continuation (2 of
AP003787 Homo sapi
AC124987 Mus muscu
AC027419 Homo sapi
AC027419 Homo sapi
AP006686 Lotus cor
AL71674 Mouse DNA
AC1373430 Rattus no
AC02539 Homo sapi
AC02589 Homo sapi
AC081827 Homo sapi
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AC103132 Rattus no
AC084394 Homo sapi
AC139292 Mus muscu
AC074391 Homo sapi
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AC098891 Rattus no
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1 (bases 1 to 723)

Gray,J., Collins,C., Hwang,S.-i., Godfrey,T., Kowbel,D. and Rommens,J.

Romens,J.

Romens,J.

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Romens,J.

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                                                                                                                                                                                                                                                                                                                                                                                            DNA
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1. .723
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Sequence 2 from patent US 5892010.
AR070325
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AY084558
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AC1125927
AC124987
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AC008019
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AC127196
AC092533
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AC021963 Homo sapi
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BD660529 Secreted
CQ776693 Sequence
AR371889 Sequence
AR371889 Sequence
AR41260 Homo sapi
BD085735 Genes fro
AC126535 Rattus no
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AL928812 Mouse DNA
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723
1 TGGAAGCTGTCATGGTTACC......TGAATGGAATATGGATTGCG 723
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163196)
6 Garay, W. W. Collins, C., Kimmerly, W., Bondoc, M., Cheng, J.,
Connolly, K.S., Gunning, K.M., Kadner, K., Miguel, T., Miller, C.,
Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                                                 TITCTAGACAGGCCAAAIGTAATTCACCTACGTGGCAGATTAAAGAGGTGGGCTTACTAG 120
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Homo sapiens chromosome 20, BAC clone
     99.9%; Score 722.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray,J.W., Collins,C.C., Hwang,S.I., Godfrey,T., Kowbel,D. and Rommens,J.
                                                   ATAGATTCAAAACTGTAGCTACTATGTGGACAGGGGGGGCAGCAAGGACCCCACTTTGTAA
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THE REGENTS OF THE UNIVERSITY OF CALIFORNIA OS Artificial Sequence PN JP 2001524802-A/2 PD 04-DEC-2001
PP 15-JUL-1997 JP 1998506264
PR 15-JUL-1996 US 08/680395, 16-OCT-1996 US 17-JAN-1997 US 08/785532
PI JOE W GRAY, COLIN CONRAD COLLINS, SOO IN HWA
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JOHANNA ROWMENS
C12N15/11,C12Q1/68,A61K48/00
Description of Artificial Sequence:1b11
Location/Qualifiers
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JP 2001524802-A/2.
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540 540 9 99 9 720 us-08-731-499-2.rge

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/note="GRAIL 2 excellent exon, frame 1" 75261) join(61724. .181846,71524. .71319,75055. .75261) frameard name="af74801" fnote="100" identity_dbEST:AA644590"
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28734. .29019
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30266. .30455
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30789. .30888
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31841. .31972
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32270. .32290
/note="(TS21"
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3268. .33474

// Note="GRAIL 2 excellent exon, frame 0"

// Ancte="(GT)14"
                                                                                                                                                                                                                                                                                                                                                                                 /rpt_unit="gt"
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43253. 43465
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complement (50487. 50600)
/rpc family="1"
50605. 50855
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prim_transcript join(75199. .75323,84601. .84746)
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72072. 72255
/rpt family="MIR"
complement (72260. 72340)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / complement (55490. 55796)
/rpt family="Alu"
55900. 56027
/rpt family="MIR"
complement (61007. 61096)
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51461. .51822
/rpt_family="THE1"
complement(54343. .5
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complement (65258. .
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fypt_unlt="t"
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69537..69618
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complement(70542.
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/rpt_unit="t"
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/note="(T)27"
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Gray, J.W., Collins, C., Kimmerly, W., Bondoc, M., Cheng, J.,
Gray, J.W., Collins, C., Kimmerly, W., Bavis, C.A., Kadner, K., Mignel, T.,
Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
Direct Submitssion
Submitted (01-JUL-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
                                                 Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
Unpublished
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omplement(16891. .17025)
rpt_family="Alu"
omplement[77221. .17682)
rpt_family="L1"
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omplement(18909. .19161)
note="GRAIL 2 excellent exon,
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/rpt_family="L1"
/rpt_family="L1"
/rpt_family="L1"
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rpt_family="Alu"
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complement (25538. .25679)
/rpt_family="MIR"
complement (26920. .27577)
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          Sequencing of human chromosome 20
                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322. .7441
rpt family="Tigger1"
omplement (8695. .9257)
rpt_family="MLT2B2"
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4588. 4709
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/rpt_family="Tiggerl"
/rpt_family="Tiggerl"
complement (6838. 77220)
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Location/Qualifiers
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family="Alu"
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5911. .15962
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                                                                                                                                                                                                                                                                                                                                                                                                                      clone="BAC 99"
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                                          (bases 1 to 163196)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bodukhay, L., Boukhayler, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Domino, M., Doyle, M., Doyle, M., Galagan, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Farzhugh, M., Forrest, C., Gage, D., Galagan, J., Rowland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levins, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, M., Meneus, E., McCurk, A., McKernan, K., McChand, C., Connor, T., O'Donnall, P., Olivar, T. M., Peterson, K., Pierre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Subrises, C., Subrama, Tana, Tana, Tonier, For Ganger, Direct Subrises, C., Subrama, Tana, Tana, Tana, Tonier, For Ganger, C., E., E., Subrama, C., Connor, C., Conno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC021963 181313 bp DNA linear HTG 16-MAR-2000
Homo sapiens chromosome 20 clone RP11-469D15 map 20, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
     421 GTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTACAA 480
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    GAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAATGGTAAGCCCCTTA
                                                                                                                                                                                                                                                        61859 circcagialadgaaacciaagalacciagagdgdgcirciggaacaarggcrcargcc
                                                                                                                                                                                                                                                                                                                                                                                                                                         661 ACAGGTAGTAGGAGACATAATTGTAGCTGGTGTGTATGGAATGTGAATGGAATATGGATT
                                                                                                             481 ACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGA
                                                                                                                                          CTTCCAGTATAGGAAACCTAAGATACCTAGAGCGGCTTTTGGGAACAATGGGCTCATGCC
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------ Project Information
Center project name: L6066
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 20, clone RP11-469D15
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Web site: http://www-seq.wi.mit.edu
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AC021963.3 GI:7249250
HTG; HTGS_PHASE1; HTGS_DRAFT.
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/note="90% identity dbEST:H88501"
join(85165. 85589,86249. 86579,87354. 87476)
/standd_name="yg09002"
/note="97% identity dbEST:R43020"
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                                                                                                                                                                                    / standard name="ym20b03"
/ note="97% identity dbBST:H15040"
/ 19526. 79590
/ standard name="nc17d10"
/ note="81% identity dbBST:AA259187"
/ complement (81547. 81627)
/ rpt family="MIR"
82700. 892865
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/rpt_family="Alu"
prim_transcript complement (84402. .84774)
/standard_name="nil4bl2"
/note="98% identity dbEST:AA554549"
prim_transcript complement (85065. .85162)
/standard_name="zm96b07"
/note="96%_identity_dbEST:AA079436"
complement(77059. .77202)
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Pred. No. 6.2e-190;
2; Mismatches 4;
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join(78685. 79043,88203. 88578)
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83191. .83347
/rpt family="Lu"
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Best Local Similarity 99.2%;
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                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center clone name: 469_D_15

Sequencing vector: M13, M77815, 100% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 172037 bases at least Q40
Consensus quality: 17874 bases at least Q30
Consensus quality: 178410 bases at least Q30
Insert size: 188000; agarose-fp
Insert size: 189503; awn-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
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102833: contrig of 14126 bp in length
102933: contrig of 24214 bp in length
127247: contrig of 24214 bp in length
127647: gap of 100 bp
150661: gap of 100 bp
181313: contrig of 3314 bp in length
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of 1797 bp in length
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Clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
/chromosome="20"
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1474: gap of 1
3271: contig c
3371: gap of 1
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                                      /note="assembly_fragment"
|1506. 15528
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|5729. 18099
|/note="assembly_fragment"
                                                                                                                                                                                               18200._.21769
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21870. .25732
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                            1719. .3686
note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment"
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note="assembly_fragment"
27248. .150561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="assembly_fragment"
|50662. .181313
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                                                                                                                                                                                                                                                                                   25833. .31618
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38708. .102833
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8779. .11405
                                                                                                                                                        clone_end:T7
vector_side:left"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8129. .72476
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Best Local Similarity 99.15
Matches 574; Conservative
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1298 ATGTGGTGTGTGAGTCACCAGTAGAGTTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 ATGIGGIGIGIGAGICACCAGIAGAGITATAAAGICCAAGGAAGIAGAATCAGCCITAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strandedness:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhara, K.
Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
Patent: EP 1394274-A 379 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
                                                          7 10-APR-1998 JP 1998543070

8 10-APR-1997 US 08/837312

1 KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, DAVID MERBERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 AAACAGTGGACCTCAACGAAGGAGAGTGCTGCACCTGAAACCCACWGAAGCGAAACTCAAAA
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                                                                                                                                     PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC St Double;
                                                                                                                                                                                                                                                                                                                                                                           Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                    Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                       Score 167.6; DB 6
Pred. No. 7.1e-36;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQ776693 2813 bp | Sequence 379 from Patent EP1394274.
                                                                                                                                                                                                                                                          1. .349
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                                                                                                                                                                                                                                    Location/Qualifiers
                      JP 2001518793-A/889
16-OCT-2001
GENETICS INSTITUTE INC
PN JP 2001518793-A/889
PD 16-OCT-2001
PF 10-APR-1997 US
PR 10-APR-1997 US
PI KENNETH JACOBS, JOHN
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                                                                                                                                                                                                  Topology: Linear;
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Best Local Similarity 98.2%;
Matches 167; Conservative ;
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CQ776693
LOCUS
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                          COMMENT
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                                            37065 ACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGGGAAACTCAAAAGA 37006
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 ATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGC 527
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 CAAAATAATCCAGGTGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGA
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Secreted expressed sequence tags (BESTs)
Patent: JP 2001518793-A 889 16-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%; Score 169; DB 6; Length 2808; 95.0%; Pred. No. 2.6e-36; cive 2; Mismatches 7; Indels
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                                                                                                                                                                                                                                          linear
                                                                                                                         37005 GAAGAAAGCAAAACCACTCTCTGATGGCGTTTCTC 36967
                                                                                                     541 GAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTC 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 02068579-A 12402 06-SEP-2002;
PE Corporation (NY) (US)
                                                                                                                                                                                                                                      2808 bp DNA
Sequence 12402 from Patent WO02068579.
CQ726468
CQ726468.1 GI:42289602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corporation (NY) (US)
Location/Qualifiers
1. .2808
/organism="Homo sapiens"
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JP 2001518793-A/889.
                                                                                                                                                                                                                                                                                                                                       sapiens (human)
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Zea mays
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Best Local &
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ACCESSION
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CQ726468
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EHQDKVDEVPGLSGQSDDVPAGKDIVDGKEKEGQELGTADCSVPGDPEGLETÄKDDSQ
AAAIAENNNSIMSFFKTLVSPNKAETKKDPEDTGAEKSPTTSADLKSDKANFTSQETQ
GAGKNSKGCNPSGHTQSVTTPEPAKEGTKEKSGPTSLPLGKLFWKKSVKEDSVPTGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENVVCESPVEIIKSKĒVESALQTVDLNEGDAAPEPTEAKLKREESKPRTSLMAFLRQM
SVKGDGGITHSEEINGKDSSCQTSDSTEKTITPPEPEPTGAPQKGKEGSSKDKKSAAB
MNKQKSNKQEAKEPAQCTEQATVDTNSLQNGDKLQKRPEKRQQSLGGFFKGLGPKRML
                                                                                                                                                                                                                                                                                                                                                                                                                         LEEVDLGISVKTDNVATSSPETTEISAVADANGKNLGKEAKPEAPAAKSRFFLMLSRP
VPGRTGDQAADSSLGSVKLDVSSNKAPANKOPSESWTLPVAAGPGQDTDKTPGHAPAQ
                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mGNOMSVPORVEDOENEPEAETYODNASALNGVPVVVSTHTVOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKVLSAARDPTLLPPETGGAGGEAPSKPKDSSFFDKFFKLDKGQEKVPGDSQQEAKRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray, J.W., Collins, C.C., Hwang, S.I., Godfrey, T., Kowbel, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                   'note="amplified and overexpressed in breast cancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2813;
    Laboratory, 1 Cyclotron Road, Berkeley, CA 94720, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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15-JUL-1996 US 08/680395,16-OCT-1996 US
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Genes from the 20q13 amplicon and their uses.
BD085735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     General from the 20q13 amplicon and their uses Patent: JP 2001524802-A 11 04-DEC-2001;
THE RECENTS OF THE UNIVERSITY OF CALIFORNIA OS Artificial Sequence PN JP 2001524802-A/11
PD 04-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.2%; Score 167.6; DB 9; 98.2%; Pred. No. 6.4e-36; ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences.
1 (bases 1 to 3066)
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                                                                                                                                                                                                              gene="AIBC1"
                                                                                                                                                                                                                                        118. .1872
/gene="AIBC1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR 15-JUL-1996 US
17-JAN-1997 US 08
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synthetic construct
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Best Local Similarity 98.2
Matches 167; Conservative
                                                    .2813
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BD085735
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                                                                                                                                                                                                                                      SBS
                            FEATURES
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Collins.C., Romens,J.M., Kowbel,D., Godfrey,T., Tanner,M.,
Hwang,S.T.: Polikoff,D., Nonet,G., Cochran,J., Myambo,K.,
Jay,K.E., Froula,J., Cloutier,T., Kuo,W.-L., Yaswen,P., Dairkee,S.,
Godvanola,J., Hutchinson,G.B., Isola,J., Kallioniemi,O.-P.,
Palazzolo,M., Martin,C., Ericsson,C., Pinkel,D., Albertson,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1358 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGGGAAACTCAAAA 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 2813)
Collino, C., Rommens, J.M., Kowbel, D., Godfrey, T., Tanner, M., Hwang, S.-I., Polikoff, D., Nonet, G., Cochran, J., Myambo, K., Jay, K.B., Froula, J., Cloutier, T., Kuo, W.-L., Yaswen, P., Dairkee, S., Giovanola, J., Hutchinson, G.B., Isola, J., Kallioniemi, O.-P., Li, W.-B. and Gray, J.W.
Palazzolo, M., Martin, C., Ericsson, C., Pinkel, D., Albertson, D., Li, W.-B. and Gray, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 AGGIGGIGIGGAGTCACCAGTAGAGATTATAAAGICCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
1418 GAGAAGAAAGCAAACCAAGAACTCTCTGATGGCGTTTCTCAGACAAATG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAAGAAAGCAAACCACTCTCTGATGGCGTTTCTCAGACAAATG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 167.6; DB 6; Length 2813;
Pred. No. 6.4e-36;
2; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and overexpressed in breast carcinoma
Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8703-8708 (1998)
98337979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arv41260 2813 bp mRNA linear
Homo sapiens AIBC1 (AIBC1) mRNA, complete cds.
AF041260
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2813)
Cowsert, L. M. and Freier, S. M.
Antisense modulation of BCAS1 expression
Patent: US 6395544-A 3 28-MAY-2002;
Location/Qualifiers
                                                                                                                                          DNA
                                                                                                                                   Sequence 3 from patent US 6395544. AR371889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
                                                                                                                                                                                                           AR371889.1 GI:34608999
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Best Local Similarity 98.2
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                         Unclassified.
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Banderen, V., Banderanaike, D., Barber, M., Barasted, M., Benahmed, F., Baldwin, D., Bander, D., Barber, M., Barasted, M., Benahmed, F., Bryant, N., Bankay, C., Burch, P., Burrell, K., Canderon, E., Carter, K., Chan, G., Chan, Y., Chen, Z., Chacko, J., Chavez, D., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermo, C., Dinh, H., Divya, K., Franger, H., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Pinley, M., Flaggi, N., Forbes, L., Foster, M., Guevara, M., Gunarane, E., Hall, M., Ganta, R., Garria, A., Garrer, M., Guevara, W., Gunaraten, P., Haaland, M., Handl, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hunes, S., Hladm, S.L., Hodgson, A., Hollins, B., Howells, S., Hladm, S.L., Hodgson, A., Hollins, B., Howells, S., Hadm, Y., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Louseged, H., Lozado, R., Lu, X., Ma, J., Mahenba, L., Loulseged, H., Lozado, R., Lu, X., Ma, J., Mahenba, M., Mahiney, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Wartin, R., Martinez, E., Mahenbari, M., Mahindartne, M., Mahmoud, M., Malloy, W., Martiney, S., McCledd, M., Darris, S., Munch, M., Morris, S., Morrels, S., Munchenson, M., Martinez, E., Milosavljevic, A., Milosavljevic, A., Milosavljevic, A., Morris, S., Morris, S., Munch, M., Morris, S., Munch, M., Morris, S., Munch, M., Norris, S., Munch, M., Norris, S., Munch, M., Norris, S., Morris, S., Munch, M., Mangum, M., Morris, S., Munch, M., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lettus norvegicus clone CH230-408J13, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1433 ATGTGGTGTGTGAGTCACCAGTAGAGATTATAAAAGTCCAAGGAAGTAGAATCAGCCTTAC 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA 538
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG 588
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                                                                                                                                                                                                                                                                                                                                    Score 167.6; DB 6; Length 3066; Pred. No. 6.4e-36;
                                                                                      'organism='Artificial Sequence'.
                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Description of Artificial Sequence:1b1
Key

    .3066
    /organism="synthetic construct"

                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                          Location/Qualifiers
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KEYWORDS
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Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Polidexter,A., Popovic,D., Primus,E., Pul,L.L., Pulopper,F., Polidexter,A., Popovic,D., Primus,E., Pul,L.L., Puscay,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuers,M., Richards,S., Riggs,F., Rives,C., Rodery,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Shen,H., Shetty,J., Shvartsbern,A., Sisson,I., Sitter,C.D., Smajs,D., Shetty,J., Shvartsbern,A., Sisson,I., Sitter,C.D., Smajs,D., Sheddar,M., Sodergren,E., Song,X.-Z., Sorelle,M., Tabor,P., Taylor,C., Taylor,T., Thomas,M., Thomas,M., Thingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,S., Warren,J., Walker,M., Williams,G., Williams,G., Willsan,D., Walden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Weinsten,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Princh, S., Shalls, S., Smith,H.O., Princh, S., Shalls, S., Smith,H.O., Walder, S., Smith,H.O., Walder, S., Smith, M.O., Walder, S., Smith, 
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21703469.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequency reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consists entirely of whole genome shotgun sequence reads.

Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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2 (Dases I to 168876)
Worley, K.C.
Direct Submission
Direct Cubmission
Direct Submission
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 151329 bases at least Q40
Consensus quality: 153110 bases at least Q30
Consensus quality: 153290 bases at least Q30
Estimated insert size: 162792, sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                            1 12922: contig of 12922 bp in length
23 13022: gap of unknown length
23 15459: contig of 142437 bp in length
60 155559: gap of unknown length
60 168876: contig of 13317 bp in length.
1..168876
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Center code: BCM
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Rat Genome Sequencing Consortium.
Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Ruzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Anyalebechi, V., Aoyagi, A., Abramzon, S., Baden, H.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

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Clackol, C., Cockrell, R., Ccok, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, L.,

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Liu, J., Liu, W., Luly, S., Khan, Z., King, L., Liz, Z., Liu, J.,

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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143430 TGAGCCACCAGTAGAGACTGTAAGGCTTGAGGAAGTAGAATCCACCTTACAAACCGTGGA 143371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACUPA1145 233233 bp DNA linear HTG 09-MAY-2003 Rattus norvegicus clone CH230-2L13, WORKING DRAFT SEQUENCE, 6 unocdered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 TGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 TTGGGGGAATGTTTTGTTTTTTTTTTTTTTTTTTCTTGGCAAAATAATCCAGGTGGTGGTGTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 CCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGAGAAAGG 548
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                             19.1%; Score 137.8; DB 2; Length 168876; ilarity 73.8%; Pred. No. 1.3e-27; Conservative 2; Mismatches 59; Indels 0; (
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xref="taxon:10116"
                                                                                              /clone="CH230-408J13"
11757. .12922
                                                                                                                                                                                                                /note="wgs_contig"
15743. .16838
/note="wgs_contig"
                                                                                                                                                         /note="wgs_contig"
13023. .14162
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Matches 172; Conserv
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AC094145/c
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Submitted (199-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON MAY 9, 2003 this sequence version replaced gi:24942806.

The sequence in this assembly is a combination of BAC based reads and whole genome shockun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shockun sequence reads. Both end sequences and whole genome shockun sequence reads. Both end sequences and whole sequence
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McMeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Mencemayor, J., Moore, S., Milsosvljevic, A., Miner, G., Minja, E., Morten, S., Murphy, M., Nair, L., Nawackelmeh, O., Okwton, N., Nguyen, N., Norris, S., Parks, K., Patal, P., Paul, H., Pals, P., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Satson, I., Sitter, C. D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sutton, A., Svatel, R., Saver, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Wailson, R., Wailson, W., Wailson, R., Waiss, R., Santh, D., Von, Wainstock, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Wannerock, G. and Gibbs, R.A.
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NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Consensus quality: 210461 bases at least Q30
Consensus quality: 212871 bases at least Q20
Estimated insert aize: 217628; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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Center clone name: CH230-2L13
.... Summary Statistics
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Rat Genome Sequencing Consortium.
Direct Submission
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Worley, K.C.
Direct Submission
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organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:10090"
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP23-321B23"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6.
Location/Qualifiers
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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HTG; HTGS PHASE1.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome="2"
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Best Local Similarity 74.7%;
Matches 171; Conservative
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Unpublished
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AC084066/c
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DEFINITION
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77539 TGAGCCACCACTAGAGACTGTAAGGCTTGAGGAAGTAGAATCCACCTTACAAACCGTGGA 77480
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Submitted (30-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 2, 2003 this sequence version replaced gi:31096514.

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgum may have been used to confirm this sequence. Sequence abotgum may have been used to confirm this sequence. Sequence date from the whole genome shotgum alone has only been used where it has a phred quality of at least 30.

Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 CCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGAGAAGGAAAG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 TGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGA 488
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 199019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 233233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °,
This record will be updated with the finished sequence
                                                    89147: contig of 89147 bp in length 89247: gap of unknown length 89513: gap of 10266 bp in length 99513: gap of 10266 bp in length 113910: contig of 14297 bp in length 114010: gap of unknown length 230487: contig of 11477 bp in length 230587: gap of unknown length 232101: gap of unknown length 232101: gap of 1114 bp in length 232101: gap of 11132 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 137.8; DB 2
Pred, No. 1.2e-27;
                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CH230-2L13"
1. .1412
/note="wgs_contig"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AL928812.11 GI:31335541
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Best Local Similarity 73.8%;
Matches 172; Conservative
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VERSION
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SOURCE
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amonatation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

En: SMBL; Sw: SWISSROT; Tr: TREMBL; Wp:, WORNPEP; Information on the WORNFEP database can be found at http://www.anger.ac.uk/Projects/C_elegans/wormpop RP23-321B23 is from the RPCT-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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Mus musculus clone RP23-321D1, *** SEQUENCING IN PROGRESS ***, 29
unordered pieces.
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Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 1.1e-24;
2; Mismatches 53; Indels
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TITLE JOURNAL COMMENT

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225082 GGGTTGTTTTGTTTTGTTTTCTTATTACCTGGCAAATAATCTAGGCGGTGTGTG 225023
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Mus musculus novel amplified in breast cancer-1 mRNA, complete cds.
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Beardsley, D.I.; Kowbel, D., Lataxes, T.A., Mannino, J.M., Xin, H., Kim, W.J., Collins, C. and Brown, K.D.
Characterization of the novel amplified in breast cancer-1 (NABC1)
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Submitted (14-JAN-2003) Biochem. and Molec. Biology, LSU Health
Sciences Center, 1901 Perdido Street, New Orleans, LA 70112, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 127.4; DB 2; Length 235411; 74.7%; Pred. No. 1e-24; ive 2; Mismatches 53; Indels 3; (
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            98998: contig of 21220 bp in length 98198: gap of unknown length 113997: contig of 15789 bp in length 114897: gap of unknown length 132115: contig of 18028 bp in length 13215: gap of unknown length 160184: contig of 27969 bp in length 160184: gap of unknown length 186598: gap of unknown length 186598: gap of unknown length 186798: gap of 48613 bp in length
                                                                                                                                                                                                                                            Location/Qualifiers
1. .235411
.0rganism="Mus musculus"
/organism="Mus musculus"
/mol_type="genomic DNA"
/db xref="texon:10090"
/dbome="genomic DNA"
/clone="lib="RPCI mouse BAC library 23"
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/note="NABC1; AIBC1; BCAS1"
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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VERSION
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PUBMED
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AUTHORS
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                                                                                                                                                                                                                                                   Consensus quality: 214207 bases at least Q40
Consensus quality: 223053 bases at least Q30
Consensus quality: 225068 bases at least Q30
Consensus quality: 225208 bases at least Q30
Estimated insert size: 200000; pulse field gel estimation
Estimated insert size: 200000; pulse field gel estimation
Guality coverage: 9.94 in Q20 bases; pulse field gel estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
Direct Submission
Submitted (12-OCT-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Web Bite: http://www.jgi.doe.gov
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/db_xxef="G1:29648618"
/db_x
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ORIGIN

1374 ATACACTTTCCACAGGTGCAGAGGAGAACGCGGTGTGTGAGTCACCAGTAGAGACCGTAA 1433 1434 GGCTTGAGGAAGTAGAATCCAGCTTACAAACTGTGGATCTCAGTGA---AGAGACCCAGC 1490 1314 Addendececchectractaccechegaaagrieririgaaagaagaagiraaagagg 1373 332 AGGGGGCAGCAAGGACCCCACTTTGTAAAACATGTTTTGGGGGAATGTTTTGTTTTCA 391 452 AGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGAAGTGCTGCAC 511 392 ITITCTTATTACCTGGCAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAA 451 Gaps 3; Query Match
12.0%; Score 86.6; DB 10; Length 2916;
Best Local Similarity 60.7%; Pred. No. 3.9e-13;
Matches 156; Conservative 2; Mismatches 96; Indels 3; 572 CGITICICAGACAAIG 588 g ò Dp g g ò ò ò

Search completed: May 5, 2005, 03:58:10 Job time : 3543.14 secs

1551 CGTTTCTCAGACAATG 1567

Ada71938 Rice gene Abx40026 Human che Acn45080 Mouse gen Abv25280 Human pro Acn44010 Human pol Acn44010 Human gen Ach67256 Human gen Adf89281 P gene Be Adj97169 P gene Be Adj97169 P gene Be Adj07820 P gene fr Adm67640 Human met Adm67640 Human met Adm67640 Human met Adf88922 Human met Adf88922 Human met Adj6810 Human met Adj6810 Human met Adm67281 Human met Adm6733 Human met Adm67281 Human met Adm6731 Human met Adm6731 Human met Adm6731 Human met Adm6731 Human fet Adm6731 Human fet Adm6731 Human fet Adm67317 Human fet Adm67317 Human fet Adm673177 Human ces

ACN45080 ABV27806 ABV25280 AA188208 ACN44010 ACH67256 ADF68708

ADJ97169 ADL07820 ADM67640

ABL29804

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The sequence is that of a cDNA sequence 1b11, which was isolated from the 20q13 amplicon. Its expression shows high correlation with the copy number of the amplicon. It can be used as a probe for the detection of chromosomal abnormalities at 20q13. It and other sequences isolated from
                                                                                                                                                                                                                                                                                                                                          20q13 amplicon; chromosome 20; tumour; detection;
chromosomal abnormalities; probe; gene therapy; antisense inhibition;
treatment; age-related macular degeneration; retinitis pigmentation;
Leber's congenital amaurosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New sequences from the 20q13 amplicon - used abnormalities, particularly tumours, and for treating diseases.
                                                                                                                                                                                                                                                                                                                          Homo sapiens 20q13 amplicon 1b11 transcript.
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96US-00731499.
97US-00785532.
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Acc90605 Human CGD
Abx44866 Bovine ES
Adg52268 Novel can
Abz13040 Arabidops
Aac50675 Arabidops
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Aa881115 DNA encod
Aad38092 Human BCA
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Adq18993 Human 80f
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(c) 1993 - 2005 Compugen Ltd.
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Rommens

Kowbel D,

Godfrey T,

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sequences are useful as probes or as probe targets for monitoring the relative copy number of corresponding sequences from a biological sample such as tumour cells. The sequences can also be used in therapeutic applications for modulating the expression of the endogenous gene or the activity of the gene product. Examples of therapeutic approaches include antisense inhibition of gene expression, gene therapy, and monoclonal antibodies that specifically bind the gene products. The products can also be used in the treatment of other diseases, e.g. age-related macular degeneration, Leber's congenital amaurosis and retinitis pigmentation
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20q13 amplicon are consistently amplified in primary tumours.
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                                                                                                                                                                                                                                         Length 723;
                                                                                                                                                                                                      Sequence 723 BP; 210 A; 138 C; 178 G; 195 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                       99.9%; Score 722.2; DB 2;
100.0%; Pred. No. 1.2e-222;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 723; Conservative
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AAV88411 standard; cDNA; 349 BP.

RESULT 2 AAV88411 ID AAV8

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The present sequence represents an expressed sequence tag (BST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted BST sequences isolated from a variety of human tissue sources. The BST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, tissue growth activity, haemostatic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                        Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                      pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACAGAAGCGAAACTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AGGIGGIGIGIGAGICACCAGTAGAGATTATAAAGICCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 ATGTGGTGTGTGACTACAGTAGAGTTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
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                                                                                                                                                                                                                                                                                                                                                                              Treacy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 GAGAAGAAAGCAAACCAAGAACCTCTGATGRCGTTTCTCAGACAAATG
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                                                                                                                                                                                                                                                                                                                                                                            Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.2%; Score 167.6; DB 2, 98.2%; Pred. No. 2.5e-43; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                              Racie LA,
                                                                                                                                                                                                                                                                                                                                                                              ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 388; 641pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Mccoy JM, Lavallie
/, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS81115 standard; cDNA; 2813
                                                                                                                                                                                                                                                                                   98WO-US006956
                                                                                                                                                                                                                                                                                                                  97US-00837312
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070078/06.
                                                                          EST clone EK480
                                                                                                                                                                                                                                                                                                                                                                              Jacobs K, Mc
Spaulding V,
                                                                                                                                                                                                                                                                                   10-APR-1998;
                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                  10-APR-1997;
                                                                                                                                                                                                                     WO9845437-A2
                                           12-FEB-1999
                                                                                                                                                                                                                                                    15-0CT-1998
              AAV88411;
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Matches
                                                                                                                                                                                      Homo
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AAS81115
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BP.

AAD38092 standard; DNA; 2813

RESULT 4

AAD38092;

(first entry)

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DNA encoding novel human diagnostic protein #16919.
 13-FEB-2002 (first entry)
                                                       biodiversity.
               Homo sapiens
                      11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The intention relates to isolated polymicisculae (ii) and polypeptide (iii) related to isolated polymicisculae (ii) and polypeptide (iii) reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymicisculaes are also used in diagnostics as expressed sequence tags for identifying expressed central in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging (iii) else expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymicleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention of the invention o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 GAGAAGAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 167.6; DB 5; Lews...
Pred. No. 7.6e-43;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 16919; 103pp; English.
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98.2%;
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                      WO200175067-A2
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1358 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACAGAAGCGAAACTCAAAA 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense compounds, compositions and methods for modulating the expression of BCASI (breast cancer amplified sequence 1, also known as AIBCI for amplified in breast cancer I and NABCI for novel amplified in breast cancer I). The antisense compounds of the invention are useful for treating an animal having a disease or condition breast or prostate cancer I). The antisense compounds of the reagents and diagnostics; to distinguish between functions of various members of a biological pathway; in the treatment of a disease or distinguish between functions of various disorder, which can be treated by modulating the expression of BCASI; as prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation; and as probes or primers. These entisense compounds are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; BCAS1; breast cancer amplified sequence 1; AIBC1; inflammation; mapplified in breast cancer 1; NABC1; novel amplified in breast cancer 1; hyperproliferative disorder; breast; prostate; cancer; prophylaxis; hyperproliferative therapy; cytostatic; antiinflammatory; tumour; gene; infection; antisense therapy; cytostatic; antiinflammatory; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compounds targeted to a nucleic acid molecule encoding BCASI, useful for treating diseases or conditions associated with BCASI, such as hyperproliferative disease, particularly breast or prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in antisense therapy. The present sequence is human BCAS1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2813 BP; 868 A; 671 C; 758 G; 516 T; 0 U; 0 Other;
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                                                                   Human BCAS1 (breast cancer amplified sequence 1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human BCAS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.6e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 92-95; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39-OCT-2001; 2001WO-US031484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2000; 2000US-00689255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.28;
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowsert LM, Freier SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-444179/47.
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002
                                                                                                                                                  Human; BCA
amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Sequence 2813 BP; 868 A; 671 C; 758 G; 516 T; 0 U; 0 Other;

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bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                1418 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
GAGAAGAAAGCAAACCAAGAACCTCTCAATGRCGTTTCTCAGACAAATG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagai H, Izuhara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohtani N, Sugita Y, Yamaya M, Kubo H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 379; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; marker gene; gene; ds
                                                                                                                                                                                                                ADJ75127 standard; DNA; 2813 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                                                                                                                                                                                                                                                                                                                          20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Marker gene SEQ ID NO:379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-193155/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          healthy subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1394274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                             ADJ75127;
539
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ADJ75127
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13, and the argority of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13, and obstructive pulmonary disease; (C2) a kit for screening for a candidate compound for a therapeutic agent (C2) a kit for screening for bronchial asthma or chronic obstructive pulmonary disease; (4) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene aribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a probe has been immobilised to assay a marker gene. (1) has restiratory and antisathmatic activites, and can be used in gene therapy. The method is subsetul for testing for or screening for a therapeutic agent in obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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Length 2813;

DB 12;

23.2%; Score 167.6;

Query Match

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                                                                                                                 1298 ATGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 1357
                                                                                                                                                                                            1358 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGCGAAACTCAAAA 1417
                                                                             478
                                                                                                                                                          538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for detecting soft tissue sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of a gene in both samples, where a higher level of protein expression in the first soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                          419 AGGIGGIGIGIGAGICACCAGIAGAGITATAAAGICCAAGGAAGIAGAATCAGCCTIAC
                                                                                                                                                            479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA
                                      Gaps
                                                                                                                                                                                                                                                       1418 GAGAAGAAAGCAAAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
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DB 12; Length 2813;
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Score 167.6; DB 12; Length
Pred. No. 7.6e-43;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human soft tissue sarcoma-upregulated DNA - SEQ ID 1812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                          ADQ18993 standard; DNA; 2813 BP
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  23.2%;
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                      Best_Local Similarity 98.2
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-441208/41.
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    Query Match
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AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACAGAAGCGGAAACTCAAAA 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1433 ATGTGGTGTGTGACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                                                                                  20q13 amplicon, chromosome 20, tumour, detection, chromosomal abnormalities; probe, gene therapy, antisense inhibition; treatment, age-related macular degeneration; retinitis pigmentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAAGTCCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abnormalities, particularly tumours, and for developing chromosometreating diseases.
                                                                                                1418 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 3066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.9e-43;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                   Homo sapiens 20q13 amplicon 1b1 transcript.
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                                                                                                                                                                                                                                                                                                                                                                                          Leber's congenital amaurosis; ds.
                                                                                                                                                                                           AAV09025 standard; cDNA; 3066 BP
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96US-00731499.
97US-00785532.
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                                                                                                                                                                                                                                                                 21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-1998
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                               1358
                                                                  539
                                                                                                                                                                                                                              AAV09025;
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                                                                                                                                                         RESULT
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                                                                                                                                                         1358 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGCGAAACTCAAAA 1417
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                                                                                                    1298 ATGTGGTGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 1357
                                                                AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                       479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                1418 GAGAAGAAACCAAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
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                                                                                                                                                                                                           GAGAAGAAAGCAAACCACTCTCAGATGRCGTTTCTCAGACAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2813 BP; 868 A; 671 C; 758 G; 516 T; 0 U; 0 Other;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; breast cancer; prognosis; gene expression; diagnosis.
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            Pred. No. 7.6e-43;
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98.2%; Pred. No. 7.6e-43;
ive 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 937; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer prognosis marker #937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE-) ROSETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
98.2%; Pre-
                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                      ADR25076 standard; DNA; 2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2003; 2003US-00342887
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                               Conservative
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            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004065545-A2
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Matches 167;
                               167;
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has excoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated DNA of the invention. The current sequence is that of a human soft tissue sarcoma upregulated specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                         ch 23.2%; Score 167.6; DB 12; Length 3418; al Similarity 98.2%; Pred. No. 8.4e-43; . 167; Conservative 2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3418 BP; 1029 A; 763 C; 842 G; 669 T; 0 U; 115 Other;
                                                        GAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG
                                                                                                                                                                                                                                                                                                Human soft tissue sarcoma-upregulated DNA - SEQ ID 6167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 6167; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                    ADQ23347 standard; DNA; 3418 BP
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                                                                                                                                                                                                                                                          26-AUG-2004 (first entry)
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Best Local Similarity
Matches 167; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-441208/41.
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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The invention relates to an isolated polypeptide associated with cell growth, differentiation and death (CGDD). Also disclosed are the polypeptides. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or orditions associated with the decreased expression or over expression of CGDD. Such diseases include cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and reproductive disorders, or disorders of the placenta. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of CGDD. The CGDD or its fragments are useful in screening compounds for effectiveness as an agonist or antagonist of the polypeptides, or in altering the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human proteins associated with cell growth, differentiation, and death (CGDD), useful for diagnosing, treating and preventing diseases conditions associated with the aberrant CGDD expression e.g. cancer,
                                                                                                                                                                                                                                                    Human, cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antifinflammatory, gynaecological, cancer, atherosclerosis, epilepsy, Huntington's disease, rarcke, ADDS; allergy, placenta, reproductive, CGDD; cell growth, cell differentiation, cell death, gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Chawla NK; Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Gorvad AE; Griffin JA, Hafalia AJA, Ison CH, Kable AE, Kalafus DP; Lehr-Mason PM, Lu DAM, Marquis JP, Nguyen DB, Ramkumar J; Richardson TW, Sapperstein SK, Swarnakar A, Tang YT, Tran UK; Warren BA, Xu Y, Yao MG, Yue H, Yue H;
1466 GAGAAGAAAGCAAACAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borowsky ML, Chawla NK;
AR, Gietzen KJ, Gorvad AE;
Kable AE, Kalafus DP;
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26-0CT-2001; 2001US-0345384P.
26-0CT-2001; 2001US-0348165P.
02-NOV-2001; 2001US-0350219P.
                                                                                                   ACC90605 standard; DNA; 2020
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2001US-0328186P.
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                                                                                                                                                                                                                      Human CGDD-28 encoding DNA
                                                                                                                                                                               (first entry)
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P-PSDB; ABR69628.
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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05-OCT-2001;
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                                                                                                                                         ACC90605;
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539 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG 588

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479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA

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Matches
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                                                                                                                                                                                                                                                                                                                     478
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1372 AAACAGTGGACCTCAACGAAGGAGATGCTGCTCCTGAACCCCACAGAAGCGAAACTCAAAA 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. Microarrays consisting polynucleotides of the invention are useful in monitoring or measuring protein-protein interactions, drug-taractions, and gene expression profiles. Sequences given in records ACC90578-ACC90634 represent polynucleotides encoding CGDD proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; lactation; LMFD; 1, fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                   419 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1432 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1481
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                                                                                                                                                                                                                   Score 166; DB 8; Length 2020;
Pred. No. 2.1e-42;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAAGAAAGCAAACCACTCTCTGATGRCGTTTCTCAGACAAATG
                                                                                                                                                                      Sequence 2020 BP; 621 A; 525 C; 529 G; 345 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX44866 standard; cDNA; 383
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23.0%;
Best Local Similarity 97.6%;
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-110599/10.
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(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002137139-A1.
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tunctions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) actecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or complement fermine then be present sequence is one of the construct may not shown in the specification but was obtained in present sequence was not shown in the specification but was obtained in the present sequence man in the specification but was obtained in a power of the construct format from the USPT (expressed sequence was not shown in the specification but was obtained in the specification and sequence in the specification but was obtained in the specification but was obtained in the specification but was obtained in the specification was obtained in the specification was obtained in the specification and sequence in the sequence was not shown in the specification was obtained the sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 ATAAAGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGACCT----CAACGAAGGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 ITCATITICITATIACCIGGCAAAATAAICCAGGIGGIGGIGGIGAGACACCAGTAGAGAIT
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environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 383 BP; 123 A; 95 C; 108 G; 56 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel canine microarray-related DNA sequence SeqID4570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88.6; DB 8;
Pred. No. 9.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TCCCTGATGGCGCTCCTCAGACAGATG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTCTGATGRCGTTTCTCAGACAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%;
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Arabidopsis thaliana.
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                                                                                                                                                                                                                    This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic caid sequences of the invention may be useful for drug screening and toxicity assays. The invention may be useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a call or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that modulate gene expression or activity. The database is useful for producing electronic Northerns that allow the user to determine the cell type or tissue in which agiven gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the likelihood that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver controls protein adduct formation or hepatitis), those of the kidney, and the second or the pathologies protein adduct formation or hepatitis), those of the kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart, brain or testes, or other pathologies associated with at least one of the toxins. The methods are also useful for predicting or elucidating the potential callular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTAAAACTCAAAAGAGAAGAATACAAACCACGAGAACATCCCTGATGGCGTTTCTCAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCAGNNNTACAAACAGTNGATCTCAATGAAGAAGAGAGATGCCACAANNTGAACCCACAGAN 60
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Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 TCAGCCTTACAAACAGTGGACCTCA---ACGAAGGAGATGCTGCACCTGAACCCACWGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 GCGAAACTCAAAAGAGAAAGCAAACCA---AGAACCTCTCTGATGRCGTTTCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                              New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell living organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Match 9.7%; Score 70.2; DB 13; Length 540; Local Similarity 80.2%; Pred. No. 1.1e-11; les 101; Conservative 2; Mismatches 17; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 540 BP; 167 A; 137 C; 140 G; 74 T; 0 U; 22 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana stress regulated gene SEQ ID NO 845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of a canine microarray of the invention.
                                                                                                                                                                                           Claim 1; SEQ ID NO 4570; 41pp; English.
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                                  Wei T;
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 (PFIZ ) PFIZER PROD INC
                                    Diggans JC, Porter M,
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                                                                     WPI; 2004-561890/54
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ABZ13040
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12195-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 regargritacacirirecacarcaacaacaacaacaacaacarcaacaaccireccaaa 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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47.2%; Pred. No. 0.035;
tive 2; Mismatches 130; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 144; SEQ ID NO 845; 577pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang X,
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                                                                                                                                                                                                              24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                         24-AUG-2001; 2001WO-US026685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harper JF, Kreps J,
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(SYGN ) SYNGENTA
WO200216655-A2
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990S-014331P.
990S-014331P.
990S-0144331P.
990S-014531P.
990S-014532P.
990S-014732P.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654 TGGCGTGCTTCAGGCTATGACGTTGAATCCAGTGTTTCAAATGATGCCATTTTGAAAGCC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTGATGRCGTTTCTCAGACAAATGGTAAGCCCCTTACTTCCAGTATAGGAAACCTAA 621
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Pred. No. 0.042;
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les 118; Conservative
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score:
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167.6
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                                                           OM nucleic
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                                                                                  Run on:
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No.
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1354, Ap
1350, Ap
2, Appli
11753, A
14219, A
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US-08-680-395-2

Sequence 2, Application US/08680395

Patent No. 5892010

APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Kowbel, David
APPLICANT: Kowbel, David
APPLICANT: Rowmens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP.
        Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
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Sequence
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transcript"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLASSIFICATION INFORMATION:
NAME: Basetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-068900US
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
US-07-667-276A-1
US-10-087-402-5
US-08-57-667-10-3
US-08-943-713-10-3
US-09-270-76-7078
US-09-270-76-7078
US-09-949-016-37900
US-09-949-016-37900
US-09-949-016-37900
US-09-949-016-37900
US-09-949-016-37900
US-09-949-016-11753
US-09-949-016-11753
US-09-949-016-11753
US-09-949-016-11751
US-09-949-016-11751
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; OTHER INFORMATION: Description of Artificial Sequence:1bl1
US-08-892-695-2
     EARLIER FILING DATE: 1997-01.17
EARLIER APPLICATION NUMBER: 08/731,499
EARLIER APPLICATION NUMBER: 08/680,395
EARLIER FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 59
SOTWMARE: PATENTIN Ver. 2.0
EARLIER APPLICATION NUMBER: 08/785,532
                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                               Gaps
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          723;
          Length
                              Indels
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US-08-892-695-2

i Sequence 2, Application US/08892695A

Patent No. 6808878

GENERAL INFORMATION:
APPLICANT: Gray, JOG W

APPLICANT: Hwang, Soo In

APPLICANT: Godfrey, Tony
APPLICANT: Rowel, David
APPLICANT: Rowel, David

TITLE OF INVENTION: GENES FROM THE 20Q13 AMPLICON AND
FILE REFERENCE: 2500-1134US3

CURRENT APPLICATION NUMBER: US/08/892,695A

CURRENT FILING DATE: 1997-07-15
         Query Match 99.9%; Score 722.2; DB 2; Best Local Similarity 100.0%; Pred. No. 3.1e-228; Matches 723; Conservative 0; Mismatches 0;
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                                   Gaps
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0
 Length
                              Indels
99.9%; Score 722.2; DB 4;
100.0%; Pred. No. 3.1e-228;
ative 0; Mismatches 0;
 Query Match
Best Local Similarity 100.
Matches 723; Conservative
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AND THEIR

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US-09-949-016-16050
; Sequence 16050, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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Matches 716; Conservative
                                                                   105767 ĠĊ 105768
                                      GC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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                               FATEUR NO. SELEAS)

FATEURAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR FILING DATE: 2000-10-20

PRIOR PRICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 12273

LENGTH: 130563
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98.9%; Score 714.8; DB 4;
Best Local Similarity 99.2%; Pred. No. 1.8e-224;
Matches 716; Conservative 2; Mismatches 4;
      Sequence 12273, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
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APPLICATE: VENTER, J. Craig et al.

APPLICATE: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PALING DATE: 2000-10-03

PRIOR PALING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEASTSEQ for Windows Version 4.0

SEQ ID NO 16650

LENGTH: 131379
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Query Match
Best Local Similarity
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                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-531
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
                                                                                                   105587 GAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATGGTAAGCCCCTTA 105646
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09689255C

Patent No. 6395544

GENERAL INFORMATION:
TELE NEPART SUSAN M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF BCASI EXPRESSION
FILE REFERENCE: RTS-0171

CURRENT APPLICATION UNMBER: US/09/689,255C

CURRENT PILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 47

LENGTH: 2813
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Patent No. 6812339
GENERAL INFORMATION:
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; LOCATION: (118)...(1872)
US-09-689-255C-3
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ORGANISM: Homo sapiens
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US-09-689-255C-3
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1493 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGCGAAACTCAAAA 1552
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GENERAL INVENTALION:

APPLICANT: Collins, Collin

APPLICANT: Godfrey, Joe W

APPLICANT: Hanang, Soo In

APPLICANT: Godfrey, Tony

APPLICANT: Rowel, David

APPLICANT: Rowel, David

APPLICANT: Rowel, David

TILLE OF INVENTION: GENES FROM THE 20013 AMPLICON AND THEIR USES

TILLE REFERENCE: 2500.124/US

CURRENT FILING DATE: 1997-07-15

EARLIER APPLICATION NUMBER: 08/785,532

EARLIER PILING DATE: 1996-10-16

EARLIER PILING DATE: 1996-10-16

EARLIER PILING DATE: 1996-07-15

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PATENTIN UVEY: 2.0

SEQ ID NO 12

LENGTH: 3066
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                                                                                                                                                                                                                    Length 2813;
                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                 Score 167.6; DB 4;
Pred. No. 1.8e-44;
                                                                                                                                                                                                 23.2%; scc. No. 1.0.98.2%; Pred. No. 1.0.2; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 531
LENGTH: 2813
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; Sequence 12, Application US/08892695A
; Patent No. 6808878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 98.2
Matches 167; Conservative
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Matches 167; Conservative
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APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991

FILING DATE:

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Gaps

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure; NAME/KEY: unsure; LOCATION: (157),(175); LOCATION: (157),(175); OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknov-US-09-248-796A-3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 ATGGTAAGCCCCTTACTTCCAGTATAGGAAACCTAAGATACCTAGAGGGGGTTTTGGGAA 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  646 CAATGGGCTCATGCCACAGGTAGTAGGACACATAATTGTAGCTGGTGTGTATGGAATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THER REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 28208
SQ ID NO 3540
LENGTH: 1728
                                                       REFERENCE NOMER: 29,700
REFERENCE NOMER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3540, Application US/09248796A
Patent No. 6747137
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                                             29,768
ATTORNEY/AGENT INFORMATION:
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                     NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; IMMEDIATE SOURCE: ; CLONE: pTZgpt-F1s US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-248-796A-3540
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US-09-949-016-17508/c
  ; ORGANISM: Human
US-09-949-016-204212
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; ORGANISM: Human
US-09-949-016-4532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-949-016-4532
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Sequence 204212, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 204212

LENGTH: 601

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFWARE: FREISEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 162024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AGIGIGIGIATACTGTAATCGTGCTATTTTTTTTCATTGAACATTTTATAAACTAGAATA 389
                                                                                                    439 GTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGACCTCAACGAA 498
                                                                                                                                                   871 GAAGTGATTGAAATTTCTGATGATGTACAAGCCACAGAAGAACCAGAAGAAATCAAACAA 930
                                                                                                                                                                                                    499 GGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGAGAAGAAGCAAACCAA 556
                                                                                                                                                                                                                                          931 GTAATTGAAGAAATTGAAGAAACTGAAGAAACTGAAGAAATTGAAGAAA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 ACTITGIAAAACAIGITITGGGGGAAIGITITIGITITICAITITCITAITACCIGGCAAA
                                                      Gaps
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                                                      .;
0
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DB 4; Length 1728;
                                                   51; Indels
  Score 36; DB 4
Pred. No. 0.44;
                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Sequence 162024, Application US/09949016 Patent No. 6812339
Query Match
Best Local Similarity 55.9%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.3
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-949-016-162024/c
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US-09-949-016-204212
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US-09-949-016-162024
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Sequence 4532, Application US/09949016

j Sequence 4532, Application US/09949016

patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/0241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FLING DATE: 2000-10-03

PRIOR FLING DATE: 2000-10-03

PRIOR FLING DATE: 2000-10-03

PRIOR FLING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 4332

LENGTHARE: FREESE FREESE OF Windows Version 4.0
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Batent No. 681239
GERERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
TITLE OF INVENTION:
FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL0013N, UNBER: US/09/949,016
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                          65 AGAAATCTGAACCCTTGTGCGCTATTGGTGGGAATGTAAAATGGAGTAGCAGTATGGA 124
                                                                                                                                                                                              64
                                                                                                                                  523 GAAGCGAAACTCAAAAGAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGA
                                                                                                                                                                                              583 CAAATGGTAAGCCCCTTACTTCCAGTATAGGAAACCTAAGATACCTAGAGGCGGCTTTTGG
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0
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Pred. No. 3;
0; Mismatches 47; Indels
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AAACAGIGICATITCICAAAAICCIGGACATAGAAII 164
                                                                                                                                                                                                                                                                                                                                                                                             643 GAACAATGGGCTCATGCCACAGGTAGTAGGAGACATAATT 682
                                                            78;
   DB 4;
Score 34.8; DB Pred. No. 0.59; 1; Mismatches
   Query Match
Best Local Similarity 50.6%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.3%;
Matches 63; Conservative
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PULYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236482 AGTGTGTGTATACTGTAATCGTGCTATTTTTTATCATTGAAACATTTATAACTAGAATA 236541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                       523 GAAGCGAAACTCAAAAGAAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 CAAATGGTAAGCCCCTTACTTCCAGTATAGGAAACCTAAGATACCTAGAGCGGCTTTTGG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 ACTITICIAAAACAIGITITIGGGGGAAIGITITIGITITITICATITITICITIATIACCIGGCAAA 411
                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 238815;
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                                                                                                                                                                                                                                               ; DB 4; Length 28374;
                                                                                                                                                                                                                                                                                                      78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23465 AAACAGTGGTCATTCTCAAATCCTGGACATAGAATT 23426
                                                                                                                                                                                                                                                    Score 34.8; DB
Pred. No. 5.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.8%; Score 34.8; DB
Best Local Similarity 57.3%; Pred. No. 20;
Matches 63; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSCTWARE: FastSEQ for Windows Version 4.0
EEQ ID NO 17508
LENGTH: 28374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16274, Application US/09949016
Patent No. 6812339
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Job time : 170.759 secs
                                                                                                                                                                                                                                                       4.8%;
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.64
Matches 81, Conservative
                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16274
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LENGTH: 238815
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Sequence 845, App Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1849, App Sequence 1869, App Sequence 27819, A Sequence 186365, Sequence 186365, Sequence 186365, Sequence 261191, Sequence 244, App Sequence 241, App Sequence 279, App Sequence 379, App

379, App 379, App 379, App 379, App 379, App 20, Appl 20, Appl 20, Appl 20, Appl 20, Appl 20, Appl 20, Appl

Sequence Sequence

Sequence ,

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

Database

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APPLICANT: COLLINS, Colin
APPLICANT: HWANG, Soo-In
APPLICANT: HWANG, Soo-In
APPLICANT: KOMPENS, Tony
APPLICANT: KOWMENS, Johanna
TITLE OF INVENTION: GENES FROM THE 20q13 AMPLICON AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Thopy disk
MEDIUM TYPE: Thopy disk
COMPUTER: IBM PC compatible
COMPUTER: BAEFOLI Release #1.0, Version #1.30
SOFTWARE: PatentIN BATA:
APPLICATION NUMBER: US/08/731,499
FILING DATE: 16-CCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/680,395
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                               US-10-312-841-1

US-10-25-323A-13

US-10-25-115-13418

US-10-25-116-108

US-10-087-192-1849

US-10-087-192-1849

US-10-087-192-1849

US-10-087-192-186364

US-10-027-632-186365

US-10-027-632-186365

US-10-027-632-186365

US-10-027-632-186365

US-10-027-632-186365

US-10-027-632-186365

US-10-037-192-244

US-10-371-264-96

US-10-371-264-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08731499; Publication No. US20030148270A1 GENERAL INFORMATION: GENERAL OPPLICANT: GRAY, Joe W.
 GRAY, Joe W.
COLLINS, Colin
957
103464
3673778
                                                 408
17534
83834
83834
3353
3353
3353
559
559
559
1113
1113
19852
885
885
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13215
13215
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13215
13335
14083
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US-08-731-499-2
 35.8
35.4
35.4
   Sequence 2, Appli
Sequence 889, App
Sequence 937, App
Sequence 937, App
Sequence 137, App
Sequence 12, Appl
Sequence 6167, Ap
Sequence 6167, Ap
                                                                                                               ; Search time 993.612 Seconds
  (without alignments)
  4449.254 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  US-08-731-499-2
723
1 TGGAAGCTGTCATGGTTACC......TGAATGGAATATGGATTGCG 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                        5654200 segs, 3057283753 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                  5, 2005, 03:59:12
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Maximum DB seq length: 200000000
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722.2 167.6 167.6 167.6 167.6 167.6 167.6

Result No.

166 88.6 41.2

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189 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,520
FILING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSED SEQUENCE TAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 889:
US-10-040-739-889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED, EX
NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS:
                                                                                                                            US-10-040-739-889; Application US/10040739; Sequence 889; Application US/10040736; Publication No. US20020173635A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 937, Application US/10172118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 349 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                     McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 889
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A
     ||||
GCG 723
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US-10-172-118-937
                               721
                                                                                                         RESULT 2
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                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAGATTCAAAACTGTAGCTACTATGTGGACAGGGGGGCAGCAAGGACCCCACTTTGTAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTGATTGGGTATTGAGCATGCTCTGAATGACAGTCCCCAAAAAGGACCTCTTATCCGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGGTGCGTTGTACAACATAAGCATTACTTCTCCAAGATGTGCCTGTGTAGAAATGGTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGATTCAAAACTGTAGCTACTATGTGGACAGGGGGCAGCAAGGACCCCACTTTGTAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AACATGTTTTGGGGGAATGTTTTTGTTTTTCTTTATTACCTGGCAAATAATCCAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 GIGGIGIGIGAGICACCAGIAGAGAITAIAAAGICCAAGGAAGIAGAAICAGCCIIACAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCTAGACAGGCCAAATGTAATTCACCTACGTGGCAGATTAAAGGGGGGGTGGGCTTACTAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TTTCTAGACAGGCCAAATGTAATTCACCTACGTGGCAGATTAAAGAGGTGGGCTTACTAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.9%; Score 722.2; DB 8; Best Local Similarity 100.0%; Pred. No. 7.6e-211; Matches 723; Conservative 0; Mismatches 0;
NAME: HUREEL, .c....
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 23070-068910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -

LOCATION: 1..723
COTHER INFORMATION: /note= "cDN:

OTHER INFORMATION: transcript"
US-08-731-499-2
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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23.2%; Score 167.6; DB 13; Length 349;
Best Local Similarity 98.2%; Pred. No. 1.2e-40;
Matches 167; Conservative 2; Mismatches 1; Indels 0;

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Query Match 23.2
Best Local Similarity 98.2
Matches 167; Conservative
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US-10-723-860-1812
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                                                                                                                 APPLICANT: Mac, Mac, Mac, AppLICANT: Roberts, Chris
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFRENCE: 9301-175-999
CURRENT TRING DATE: 2002-06-14
FRIOR APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 937
LENGTH: 2813
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APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Lord, Reginald V.
APPLICANT: Averez, Chris
APPLICANT: Scherf, Jon C.
APPLICANT: Wetzel, Jon C.
APPLICANT: Wockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Bsophageal Tissue FILE REFERENCE: 4921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2001-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR PLILING DATE: 2001-03-31
PRIOR FILING DATE: 2000-03-31
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US-10-240-425-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1418 GAGAAGAAAGCAAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.2%; Score 167.6; DB 17; Length 2813; Best Local Similarity 98.2%; Pred. No. 3.4e-40; Matches 167; Conservative 2; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 003657
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 385, Application US/10240425
Publication No. US20040033502A1
  Publication No. US20030224374A1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 385
LENGTH: 2813
                                                APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linaley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Sequence 1812, Application US/10723860 ...

Bublication No. US20040253606A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Gineburg, Wendy M.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1358 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAAGCGAAACTCAAAA 1417
                                                                                                                                                                                                                                                                 419 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                419 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van t Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Unversion of Vijver, Marc J.
APPLICANT: Bernards, Rene
7 TITLE OF INVERNION: Diagnosis and Prognosis of Breast Cancer Patients
7 TITLE OF INVERNION: 2010-188-199
7 CURRENT APPLICATION NUMBER: 60/298,918
7 PRIOR APPLICATION NUMBER: 60/298,918
7 PRIOR PILING DATE: 2001-06-18
7 PRIOR FILING DATE: 2001-06-18
7 PRIOR FILING DATE: 2002-06-14
7 PRIOR FILING DATE: 2002-06-14
7 NUMBER OF SEQ ID NOS: 2699
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                                                        1; Indels
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Pred. No. 3.4e-40;
2; Mismatches 1
                                .4e-40;
                                                        2; Mismatches
Score 167.6;
Pred. No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 937, Application US/10342887 Publication No. US20040058340A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.2
Matches 167; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 3066 base pairs
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Methods for Screening for Soft Tissue Sarcoma Modulators
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US-08-731-499-12

US-08-731-499-12

Sequence 12, Application US/08731499

PUBLICATION NO. US20030148270A1

GENERAL INFORMATION:
APPLICANT: GOLLINS, Colin
APPLICANT: GOLFEX, Tony
APPLICANT: ROWBEL, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1418 GAGAAGAAAGCAAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1467
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COUNTRY: USA
ZIP: 94111-384
ZIP: 94111-384
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,499
FTLING DATE: 16-OCT-1996
FTLING DATE: 16-OCT-1996
                   FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
FRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
LENGTH: 2813
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REGISTRATION NUMBER: 38 498
REGISTRATION NUMBER: 23070-068910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/680,395
FILING DATE: 15-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-10-723-860-1812
TITLE OF INVENTION:
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Sequence 6167, Application US/10723860
Publication No. US2004025366A1
GENERAL INFORMATION:
APPLICANT: Ainsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT PILING DATE: 2002-11-26
PRIOR FILING DATE: 2002-11-26
PRIOR FILING DATE: 2002-11-26
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                                                                                                                                                                                                                                23.2%; Score 167.6; DB 8; 98.2%; Pred. No. 3.6e-40; tive 2; Mismatches 1;
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Pred. No. 3.8e-40;
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                                                                                         ; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3066
; OTHER INFORMATION: /note= "lbl"
US-08-731-499-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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SOFWARE: Patentin version 3.2
SEQ ID NO 6167
LENGTH: 3418
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Best Local Similarity 98.2%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM:
NAME:
NAME:
LOCATION: (1815) .. (1815)
OTHER INFORMATION: n is a, c
FEATURE:
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; LCCATION: (3303)..(3416)
; OTHER INFORMATION: n is a,
US-10-723-860-6167
                                                                                                                                                                                                                                  Query Match 23.2
Best Local Similarity 98.2
Matches 167; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                   MOLECULE TYPE: CDNA
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Sequence 10031, Application US/09960352
Patent No. US2002013713941
GENERAL INFORMATION:
APPLICANT: Warren, Weeley C.
APPLICANT: Byatt, John C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298) C.
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NO 10031
LENGTH: 383
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Alu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPISOO: 3
CURRENT APPLICATION NUMBER: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 ATAAAGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGACCT---CAACGAAGGAGAT 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GAGGATTCAGTCCCCACAGGTGCAGAGGAGAATGTGGTGTGTGAGTCACCAGTAGAGGCT
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                               1432 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 88.6; DB 9; Length 3 62.9%; Pred. No. 2.3e-16; tive 2; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure

; LOCATION: (336)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 43-LIB34-002-Q1-E1-C12

US-09-960-352-10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562 TCTCTGATGRCGTTTCTCAGACAATG 588
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 62.9
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                         RESULT 10
US-09-960-352-10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-938-842A-845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YUE, HENLY
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PF-1213 USN
CURRENT APPLICATION NUMBER: US/10/491,213
CURRENT FILING DATE: 2004-03-26
PRIOR FILING DATE: 2005-09-26
PRIOR PELLOGATION NUMBER: US 60/326,389
PRIOR FILING DATE: 2001-09-28
PRIOR PELLOGATION NUMBER: US 60/327,380
PRIOR PELLOGATION NUMBER: US 60/329,80
PRIOR PELLOGATION NUMBER: US 60/329,690
PRIOR PELLOGATION NUMBER: US 60/329,690
PRIOR PELLOGATION NUMBER: US 60/345,384
PRIOR PELLOGATION NUMBER: US 60/348,165
PRIOR PELLOGATION NUMBER: US 60/348,165
PRIOR PELLOGATION NUMBER: US 60/348,165
PRIOR PELLOGATION NUMBER: US 60/344,518
PRIOR PELLOGATION NUMBER: US 60/344,518
PRIOR PELLOGATION NUMBER: US 60/345,143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 114 SOFTWARE: PERL Program
1466 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGGCGTTTCTCAGACAAATG 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                           BOROWSKY, Mark L.; CHAWLA, Shanya D.;
BOROWSKY, Mark L.; CHAWLA, Narinder K.;
BLLIOTT, Vicki S.; EMERLING, Brooke M.;
GANUDHI, Amena K.; GIETZEN, Kimberly J.;
GORVAD, Ann E.; GRIFFIN, Jennifer A.;
HAFALLA, April J.A.; ISON, Craig H.;
KABLE, Amy E.; KALAFUS, Daniel P.;
KABLE, Amy E.; KALAFUS, Daniel P.;
KABLE, Amy E.; KALAFUS, Daniel B.;
MARQUIS, JOSEPH P.; NOUYEN, Danniel B.;
RAMKUMAR, Jayalaxmi; RICHARDSON, Thomas W.;
KAREHT, SCEPHANIE K.; SWARNAKAR, Anita;
TANG, Y. Tom; TRAN, Uyen K.;
WARREN, Bridget A.; XU, Yuming;
YUE, Hanryu
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; AZIMZAI, Yalda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 4757551CB1
US-10-491-213-85
                                                                                                               US-10-491-213-85
; Sequence 85, Application US/10491213
; Publication No. US20050048490A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PERL
SEQ ID NO 85
LENGTH: 2020
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APPLICANT: Epigenomics AG
TITLE OF INVENTIVO: Disagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REPERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94574 AAGGITTIATTAGGTTTTATTTAAAAATGTTTTTTATAAGATACAAGTAAATGTAGT 94515
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                                                                                                                                                                                                                                                                                                                         538 TTTCAGACGAAGTTCCGGCCACATCTTGTATTGGCACTTGATCAGGTGAAGGAAACATG 597
      502 GATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGAGAAGAAAGGAAACCAAGAACC 561
                                                                                                                                                                                                                                           562 TCTCTGATGRCGTTTCTCAGACAAATGGTAAGCCCCCTTACTTCCAGTATAGGAAACCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GGTGGGCTTACTAGATTTGATTGGGTATTGAGCATGCTCTGAATGACAGTCCCCAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94634 GATGGGCTTCATATGTATATTTGGCAAATTCTAGTGAATAGAAACACAATTTAGAAAGAG
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                                                                                                                  Length 103464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 323, Application US/1032281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REPERENCE: 529452001000
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 39.4; DB 18;
52.8%; Pred. No. 5.3;
tive 0; Mismatches 76;
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ORGANISM: Mus musculus
PEATURE:
NAME/KEY: misc_feature
LCCATION: 1)...(103464)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 52.8
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 GAGGATAAGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 GATACCTAGA 631
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LOCATION: (3294164)
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US-10-322-281-323/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 323
LENGTH: 103464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-312-841-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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Fublication No. US20040009476A9

Fublication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Kreps, Joeff

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APPLICANT: And, Xun

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APPLICANT: And, Yun

APPLICANT: And, Yun

APPLICANT: And, Yun

APPLICANT: AND, AND METHODS OF USE

FILE REPERENCE: SCRIPIAO.3

FURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

FRIOR FILING DATE: 2001-08-24

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-01-6

FRIOR FILING DATE: 2001-06-22

FRIOR FILING DATE: 2001-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 TGGCGTGCTTCAGGCTATGACGTTGAATCCAGTGTTTCAAATGATGCCATTTTGAAAGGCC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 GATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAAGAGAAGAAAGCAAACCAAGAACC 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 AGTGCAGCAACTGAGGCTATAGAGAAGATCTATCAAGGACAACAATTAGCCCAATAACT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 TCTCTGAIGRCGTTTCTCAGACAAATGGTAAGCCCCTTACTTCCAGTATAGGAAACCTAA 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
5.7%; Score 41.2; DB 9; Length 9
Best Local Similarity 47.2%; Pred. No. 0.13;
Matches 118; Conservative 2; Mismatches 130; Indels
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 845
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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US-09-938-842A-845
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-842A-845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-938-842A-845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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92 GTGGCAGATTAAAGAGTGGCCTTACTAGATTTGATTGGGTATTGAGCATGCTCTGAATG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 CCATGTCAATGTGGCAGTTGAGCTTGGAAATTGGTGCGTTGTACAACATAAGCATTACTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
5.2%; Score 37.4; DB 19; Length 4
Best Local Similarity 9.4%; Pred. No. 1.2;
Matches 36; Conservative 204; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: modified base
COCATION: (406)...(406)
US-10-275-323A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base
LOCATION: (364)..(364)
OTHER INFORMATION: a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified base LOCATION: (269)..(269) OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
LOCATION: (330)..(330)
OTHER INFORMATION: a, c, g,
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified base
LOCATION: (253)..(253)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                         NAME/KEY: modified base
LOCATION: (236)..(236)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified base
LOCATION: (355)..(355)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified base
LOCATION: (357)...(357)
OTHER INFORMATION: a, c,
                                                                                                                                NAME/KEY: modified base
LOCATION: (226)..(227)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified base LOCATION: (245) ... (\overline{2}45) OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (324)..(324)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (352)..(352)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified base
LOCATION: (362)..(362)
OTHER INFORMATION: a, c,
OTHER INFORMATION: a, c,
                                                                 LOCATION: (217)...(217)
OTHER INFORMATION: a, c,
                                            NAME/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DONNE-GOUSSE, CAROLE
APPLICANT: DONNE-GOUSSE, CAROLE
APPLICANT: DONNE-GOUSSE, CAROLE
APPLICANT: LAUDET VINCENT
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: IT OUT
FILE REFERENCE: 0.608-10.62
CURRENT FILING DATE: 2.001-0.4-26
CURRENT FILING DATE: 2.001-0.4-26
FRIOR FILING DATE: 2.001-0.4-26
FRIOR FILING DATE: 2.001-0.5-09
NUMBER OF SEQ ID NOS: 96
SSEQ ID NO 13
LENGTH: 4.08
                                                                                                                                                                          1519228 АЛААСАЛАЛАТСАЛАЛАЛАЛАЛАЛАСАССОЛОНОНОТЕСТИССТАТАСТАТАТА 1519169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA fragment amplified
OTHER INFORMATION: from the genome of birds
                                                                                                                                     410 AAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAAT 469
                                                                                                                                                                                                                           470 CAGCCTTACAAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGA 529
                                                                                                                                                                                                                                                                                                                    AACTCAAAAGAAAGAAAGCAAACCACAAGAACCTCTCTGATGRCGTTTCTCAGACAAATGG 589
                                                                                        0; Gaps
                                          Query Match 5.4%; Score 39; DB 16; Length 3673778; Best Local Similarity 48.8%; Pred. No. 44; Matches 102; Conservative 1; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1519168 CAATCCCTTTACTATCATAAAATTCACC 1519140
                                                                                                                                                                                                                                                                                                                                                                                                             TAAGCCCCTTACTTCCAGTATAGGAAACC 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-275-323A-13/c
; Sequence 13, Application US/10275323A
; Publication No. US20050079491A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified base
LOCATION: (71)..(71)
OTHER INFORMATION: a, c, g, or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: modified_base
LOCATION: (134). (134)
OTHER INFORMATION: a, c, g, or t
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LOCATION: (212)..(212)
OTHER INFORMATION: a, c, g, or t
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LOCATION: (57)..(57)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: modified base LOCATION: (43)..(43) OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified base (214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial
US-10-312-841-1
                                                                                                                                                                                                                                                                                                                      230
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159 YDGHKRAARWHYDYTGGTTKHRTTYNKDDDKYSYRDRRRWWRYRSWDRRWRDKWWDWTKK 100
                                                                                                                                     272 CTCCAAGATGTGCCTG-TGTAGAATGGTCATAGATTCAAAACTGTAGCTACTATGTGGA 330
                                          219 WDNRDNDDDDWWTDVDDKWDKDDDDKDBDDRDWWKAYRHWABRWRDWKKDWWKDHWDAW 160
                                                                                331 CAGGGGGCAGCAAGGACCCCACTTTGTAAAACATGTTTTGGGGGGAATGTTTTGTTTTTC 390
279 HHRTKHDWWYNKKWHDGWHKHKHVRVNDDWDBVWNRDDWRRSRNRWTWDDDRNNDGVRRT 220
                                                                                                                                                                                            451 AAGTCCAAGGAAGTAGAATCA 471
                                                                                                                                                                                                            : :: | :| :| :: 39 RCMWYAACYRAATGHGRHCMA 19
g
                        8 6 8 6 8 6 8 6
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Search completed: May 5, 2005, 12:12:19 Job time : 1007.61 secs

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May 4, 2005, 23:17:50 ; Search time 3060.29 Seconds (without alignments) 8992.766 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                            US-08-731-499-2
723
1 TGGAAGCTGTCATGGTTACC......TGAATGGAATATGGATTGCG 723
                                                                                                                                                                                                                                                                                                                                                                                 68479088
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                       34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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9b est2:

9b est4:

9b est4:

9b est6:

9b gs81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST: *
                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                      Run on:
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			•			SUMMARIES			
Result	ult		Query						
- 1	No.	Score		Length DB	DB	, QI	Description	uo	
U	-	384.2	53.1	504	2	BQ320066	BQ320066	PM3-CT081	
	7	169.2	23.4	5738	٣	CR749643	CR749643	Homo sapi	
	m	166	23.0	280	4	BI041215	BI041215	ILS-NT027	
	4	166	23.0	837	4	BG290366	BG290366	602388204	
	S	127.6	17.6	645	æ	BH086142	BH086142	RPCI-24-3	
ပ	9	123	17.0	381	~	AW453053	AW453053	UI-H-BW1-	
	7	122.2	16.9	394	Н	AA644590	AA644590	af74a01.r	
υ	80	104.2	14.4	416	ч	AI060049	AI060049	UI-R-C1-k	
υ	Φ	100	13.8	358	Н	AI459809	AI459809	ap17h05.x	
	10	98.8	13.7	583	9	CB586288	CB586288	AMGNNUC: N	
	11	89.8	12.4	359	7	BE485778	BE485778	172996 BA	
	12	88.2	12.2	246	~	BE477506	BE477506	161238 BA	
	13	9.98	12.0	668	4	BG964319	BG964319	602831931	
	14	96.6	12.0	892	'n	BU841356	BU841356	AGENCOURT	
	15	96.6	12.0	2339	m	AK008957	AK008957	Mus muscu	
U	16	81.4	11.3	906	~	BE305008	BE305008	600942990	
	11	66.2	9.5	905	~	BF581751	BF581751	602099533	
	18	51.4	7.1	1000	~	BF577458	BF577458	602092302	
	19	45.6	6.3	322	7	BF853823	BF853823	MR2-EN009	
	20	43.8	6.1	681	9	CB423181	CB423181	596383 MA	
	21	42.8	5.9	1341	m	CNSOADBC	BX817048	Arabidops	
	22	42.2	5.8	1208	S	BX898592	BX898592	BX898592	
U	23	41.6	5.8	879	7	BE740812	BE740812	601593011	
	24	41.4	5.7	922	4	BG961911	BG961911	602826590	

AQ934160 RPCI-23-2 BU635914 042F07 BY814814 NYSELIANDE	BX442513 BX442513 CO954055 UMC-pnata	AU6/1212 AU6/1212 CL108034 ISB1-49D4 BF691065 602247118 BI390256 DGDIC.DK0	CE248517 Figr-gss- CO879260 BovGen 07 BX133486 Danio rer	CN034417 Math pl D BH402050 A5-ND-139 CN216393 30290 Sus BH723558 BOMJV18TF	BU505079 AGENCOURT BX172820 Danio rer CN059701 Salamande AA109272 MBAFCE280 CE115637 tigr-g8s-
AQ934160 BU635914	EX442513 CO954055	AU6/1212 CL108034 BF691065 BI390256	CE248517 CO879260 BX133486	CN034417 BH402050 CN216393 BH723558	BU505079 BX172820 CN059701 AA109272 CE115637
591 8	1111 5 391 7	282 1057 9 1163 2 635 4	734 9 600 7 684 9	615 7 535 8 722 7 755 8	1302 658 722 722 722 1 202 1 689
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2.14	4.0 4.0 4.0 6.0	2000 2000 2000 2000	339.4 39.2 4.2 2.5	38 38.6 38.6	38.6 38.4 38.2 38.2
c 55	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	c 31 32 33	1 W W W	ი ი 337 40	0 0 4 4 4 4 4 10 10 10 10 10 10 10 10 10 10 10 10 10 1

ALIGNMENTS

, RESULT 1

BQ320066/c	
rocus	BQ320066 504 bp mRNA linear EST 17-MAY-2002
DEFINITION	PM3-CTOB1/-190501-005-012 CTOB1/ HOMO BAPIENB CDNA, MKNA BEQUENCE. B03-2006
VEDSTON	DV320066 1 CT.20026791
KEVWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	
	Chordata;
	Primates;
REFERENCE	1 (bases 1 to 504)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
	Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
	Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
	Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
	O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
	Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed
	sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10/3/800
COMMENT	Contact: Simpson A.J.G.
	Laboratory of Cancer Genetics
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
	Brazil
	Tel: +55-11-2704922
	Fax: +55-11-2707001
	This sequence was derived from the FAPESP/LICR Human Cancer Genome
	Project. This entry can be seen in the following URL
	(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM3&t2=PM3-CT0817-
	190501-005-d12&t3=2001-05-19&t4=1)
	Seg primer: puc 18 forward
	quality sequence start:
	High quality sequence stop: 433.
FEATURES	Location/Qualifiers
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	/db_xrer="taxon:9606"
	/acv stage="Adult"
	/note-"Order colon Vertor nucle, Site 1, Smal; Site 2,
	Amair a mini-library was made by cloning broducts derived
	political company for the contract that a finish

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/translation="SQAADKAETENNISTHEFRTLUSPUKAETKKDPEDTASKAESVCD GQAGGKTSEIQARGKKHLDSPRLGLAFRKFFRHKGAEKSPTTSADLKSDKANFTSQ GDAGGKTSEIQARGKKKKHLDSPRLGLAFRKFFRHKGAEKSPTTSADLKSDKANFTSQ ETQGAGGKNSKGCNPSGHTQSVTTPEPAKEDTKEKSGPTSLPLGKLFWKKVVCESPVEI IKSKEVESALQTVDLNEGDBAPEPTEAKLKREESKPRTSLMAFLRQMTSDSTEKTITP PEPEPTGAPQKGKEGSSKDKKSAAEMNKQKSNKQEAKEPAQCTEQATVDTNSLGNGDK LQKRRPEKRQSLGGFFKGLGPKRMLDAQVQTDPVSLGPVGKFKYTGKCVFSHVKKWP PQENSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases I to 280) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                        /clone="DKFZp686B1850"
/tissue type="amygdala"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI041215 230201-371-c12 NT0274 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                           sequence 1, N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACAGAAGCCGAAACTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 AGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                               /dev stage="adult"
/note="breast carcinoma amplified truncated, differentially spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%; Score 169.2; DB 3.
98.8%; Pred. No. 2.3e-38;
iive 2; Mismatches 0
                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical
/protein_id="CAH18437.1
/db_xref="G1:51476982"
                                                                                                     db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                               gene="DKFZp686B1850"
                                                                                                                                                                                                                                                                                                                                                                                              'gene="DKFZp686B1850"
  location/Qualifiers
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BIO41215
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Homo sapiens mRNA; cDNA DKFZp686B1850 (from clone DKFZp686B1850).
CR749643
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from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                            277
                                                                                                                                                                                                                                                                                                                                               502 CCAAGTGCCATTTGACTTTGAAATTGGGCCCTTGTACCACAATAACCCTTCTTTTCCCAA 443
                                                                                                                                                                                                                                                                                                                                                                                                   278 GATGTGCCTGTGTAGAAATGGTCATAGATTCAAAACTGTAGCTACTATGTGGACAGGGGG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AATGCCCCGGTTAAAAATGCTCATAGATTCAAAACTGTAGCTACTATGTGGACAGGGGG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 GCAGCAAGGACCCCACTTTGTAAAACATGTTTTGGGGGAATGTTTTGTTTTCATTTTCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 CAAACAAGGACCCCACTTTGTAAAACATGTTTTGGGGGAATGTTTTGTTTTTCATTTTCT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTACCTGGCAAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCA 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  637
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp6861850) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
Please contact AZPD for ordering:
Please contact Lapp for ordering:
Puther information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAAGTAGAATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAAC
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                                                                                                                                                                                                                                                                                            218 CAATGIGGCAGTIGAGCTIGGAAATIGGIGCGTIGIACAACAIAAGCAITACTICTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 TATTACCTGGCAAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAAAGTCCA
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Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                          ö
                                                                                                                                                                                    Length 504;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                 Score 384.2; DB 5;
Pred. No. 1.8e-102;
2; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 TTTGGGAACAATGGGCTCATGCCACAGGT 666
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                                                                                                       stringency conditions."
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                                                                                                                                                                                    tch 53.1%;
al Similarity 90.6%;
407; Conservative 2
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Best Local S
Matches 407
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/mol Lype="mana" aprens
/mol Lype="mana" aprens
/db xref="taxon.9606"
/dc_stage="Adult"
/clone_lib="Nr0214"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal, A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-NT0274-
230201-371-cl2&t3=2001-02-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remmil.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.h column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ATGTGGTGTGTGAGACACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIH-WGC DELETP://GG7/,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539 GAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.0%; Score 166; DB 4; Length 280; Best Local Similarity 97.6%; Pred. No. 8.8e-38; Matches 166; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                       1. .280
/organism="Homo sapiens"
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Location/Qualifiers
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Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG290366
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RPCI-24-33809.TJ RPCI-24 Mus musculus genomic clone RPCI-24-33809,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: State of the mouse BAC library RPCI-24. For BAC Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejongomail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 338 row: O column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
                                                                    /Listue_type="transitional cell papilloma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_91"
/note="forgan: bladder; Vector: pCMV-SPORT6; Site_1: NotI.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Ab. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taegaye, G., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M. Taegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-33809.TV

Contact: Shaying Zhao

Department of Bukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AGGIGGIGIGAGICACCAGIAGAGAITAIAAAGICCCAAGGAAGIAGAAICAGCCITAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA
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                                                                                                                                                                                                                                                                                                                                           23.0%; Score 166; DB 4; Length 837; llarity 97.6%; Pred. No. 1.2e-37; Conservative 2; Mismatches 2; Indels
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/strain="C57BL/6J"
                                                 /clone="IMAGE:4517041"
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/clone="RPCI-24-33809"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Linl. at:
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UI-H-BW1-ama-e-10-0-UI.81 NCI_CGAP_SUb7 Homo sapiens cDNA clone
IMAGE33069402 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
/clone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male CS7BL/6J DNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGGAATGTTTTTTTTTTTTTTTTTATTACCTGGCAAAATAATCCAGGTGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
                                                                                                                                                                                                                                                                                                                                             17.6%; Score 127.6; DB 8; 70.5%; Pred. No. 2.8e-26; ive 2; Mismatches 71;
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single-stranded DNA preparation of NCI CGAP_Sub6 was used as a tracer in a subtractive hybridization_with a driver comprising: the IMAGE Dool (NCI CGAP Kid3 pool) I LLAM 334-3337, 368-3683, 3798-3803 (IMAGE CloneIDS 1322376-1323911, 1456008-1456775,1500552-1502855); NCI CGAP Kid5 pool I LLAM 3334-372-3725, 3776-3778 (IMAGE CLONEIDS 132912-132581, 1411368-1472903, 1492104-1493255); NCI CGAP_Lu5 pool I LLAM 3575-3582, 3851-3854 (IMAGE CLONEIDS 141920-1417991, 1520904-152239); NCI CGAP_Lu5 pool I LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CLONEIDS 141920-1417991, 1520906-1258631,146906-4170983, 147520-2759, 3062-3068 (IMAGE CLONEIDS 111AAD 2457-2459, 2758-2759, 3062-3068 (IMAGE CLONEIDS 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP_COL Pool I LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CLONEIDS 2708616-7710535) and NCI CGAP_Sub1 (IMAGE CLONEIDS 2708616-7710535) and NCI CGAP_Sub1 (IMAGE CLONEIDS 2708616-7710535) and NCI CGAP_Sub1 (IMAGE CLONEIDS 270856-7712455) (104 of the driver population), plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE CLONEIDS 271285-2729325) (104 of the driver population), plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2712855-2729325) (104 of the driver population), plus a pool of 5,472 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2712856-2723359) (104 of the driver population), plus a pool of 6,402 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2733190) (40% of the driver population), plus a pool of 6,402 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2733190) (40% of the driver population), plus a pool of 6,402 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2733190) (40% of the driver population), plus a pool of 6,403 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2733190) (40% of the driver population), plus a pool of 6,403 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2733190) (40% of the driver population), plus a pool of 6,403 clones from NCI CGAP_Sub3 (IMAGE CloneIDS 2728956-2729355) (40% of the driver population), plus a pool of 6,403 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 bp mRNA linear EST 02-MAR-1998 af7401.rl Soares NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047720 AA644590
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H. (bases 1 to 194)
Hillier,L. Allen,M. Bowles,L., Dubuque,T., Geisel,G., Joet,S., Krizman,D., Kucaba,T., Lacy,M., Ie,N., Lennon,G., Marra,M., Martin,J., More,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashJ.NCI human EST Project
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAAAA
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TAG_LIB=NCI_CGAP_Brn50
TAG_SEQ=TTTCG"
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Best Local Similarity
Matches 126; Conserv
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512 CTGAACCCACWGAAGCGGAAACTCAAAAGAGAAGAAAGCAAACCAAGAACCTCTCTGATGR
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Matches
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                                                                                                                                                                                                                                                                            /Mol type="mrkNA"
// Ab xref="taxon:9606"
// Alone="INAGE:1047720"
// Clone="INAGE:1047720"
// Issue type="Pooled human melanocyte, fetal heart, and pregnant uterus"
// Issue type="Pooled human melanocyte, fetal heart, and pregnant uterus"
// Issue type="Pooled human melanocyte, fetal heart, and (See Delow); Vector: pT7T3D-Pac (PhArmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA_from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 05-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACAGAA 60
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 416)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 758 GE Error: 0.00
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 355.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 GCGAAACTCAAAAGAGAAGAAAGCAAACCAAGAACCTCTCTGATGRCGTTTCTCAGACAA
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UI-R-CI-kz-d-09-0-UI.S1 UI-R-CI Rattus norvegicus cDNA clone
UI-R-CI-kz-d-09-0-UI.3', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122.2; DB 1
Pred. No. 9.6e-25;
2; Mismatches 0
                                                                                                                                                                                                                                                             organism="Homo sapiens"
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98.4%;
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Best Local Similarity 98.49
Matches 121; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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LOCUS
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TITLE
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PUBMED
COMMENT
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                                                                                                                                                                                                                  FEATURES
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/clone_Ilde='Ul-K-Cl'
/noce="Wector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-Cl
library is a subtracted library derived from the UI-R-Cl
library, which is a subtracted library derived from the UI-R-Al and UI-R-Al library
consisted of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The UI-R-El library consisted of a mixture of
individually tagged normalized libraries constructed from
B, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Cl) was constructed as follows; PCR
amplified cDNA inserts from UI-R-CO clones from which 3'
ESTS had been derived was used as a driver in a
hybridization with the UI-R-CO library in the form of
circles (subtracted library) was purified by
circles (subtracted library) was subtricted
Email: benco-soares@uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1784646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
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library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 ITTTCTTATTACCTGGCAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%; Score 104.2; DB 1; Length 416; 62.3%; Pred. No. 2.1e-19; tive 2; Mismatches 95; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                         Seg primer: M13 Forward
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47

DEFINITION ACCESSION VERSION

REFERENCE AUTHORS

JOURNAL

TITLE COMMENT FEATURES

ORIGIN

硆 ઠે

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/mol_type="mRNA"
/db_xref="texcon:10116"
/clone="nrbhy5-00221-h3"
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/clone lib="W Rat hypothalamus (10471)"
/clone lib="W at hypothalamus (10471)"
/clone lib="W at hypothalamus adult female Wistar rat avg. īnsert size 2.3
kb fraction 6 and 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCACWGAAGCGAAACTCAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 AAACCGTGGATCTCACTGAGAAAGAAACCCAGACTGAGCCCACACAGATGTGAAAGTCAAAG 158
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                                                                                                   Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E. E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 AGGIGGIGIGIGAGICACCAGIAGAGATIAIAAAGICCAAGGAAGIAGAAICAGCCIIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 ACGCGGTGTGTGAGCCACCAGTAGAGACTGTAAGGCTTGAGGAAGTAGAATCCACCTTAC
                                                                                                                                                                                                                                                                                                                                                                 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
Plate: 00221 row: h column: 3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%; Score 98.8; DB 6; Length 583; 72.9%; Pred. No. 9.4e-18; ive 2; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, Beltsville Agricultural Research Center Bdlg, 200 Rm 2A, Beltsville, MD 20705, USA Pel: 301 504 8416 Fax: 301 504 8414 Email: tads@lpsi.barc.usda.gov
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    .583
/organism="Rattus norvegicus"

                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                                                            1 (bases 1 to 583)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                           CB586288.1 GI:29530329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE485778.1 GI:9605311
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Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Schiller oligodendroglioma"
/clone lib="Schiller oligodendroglioma"
/note="Organ: brain; Vector: pBluescript SK- (Stratagene);
Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was
prepared from human_oligodendroglioma using primer
5'-GAGAGAGAGAGAGAGAAACTAGTCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGGCAGAGA.' The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. Tumor
identification by consensus pathology; contains
chromosome lp and 19q deletion as determined by CGH. This
library was constructed by Dr. Martin Schiller (Johns
Hopkins University)."
                                                    158 bp mRNA linear EST 09-MAR-1999 apl'hN05.x1 Schiller oligodendroglioma Homo sapiens CDNA clone IMAGE:1955673 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB586288 S83 bp mRNA linear EST 03-APR-2003 AMGNNUC:NRHY5-00221-H3-A W Rat hypothalamus (10471) Rattus norvegicus cDNA clone nrhy5-00221-h3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTGGTGTGAGTCACCAGTAGAGATTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 478
                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalai, Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Bases 1 to 358)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Karzman, D., Kucaba, T., Lacy, M., Lennon, G., Marra, M., Markin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 AGGTGGTGTGTGAGTCACCAGTAGAGTTATAAAGTCCAAGGAAGTAGAATCAGCCTTAC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AAACAGTGGACCTCAACGAAGGAGATGCTGCACCTGAACCCCACWGAAGCGAAACTCAA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@mage.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="oligodendroglioma"
/dev_stage="44 years"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1955673"
                                                                                                                                                          A1459809
A1459809.1 GI:4312690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                       Homo sapiens (human)
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CB586288
LOCUS
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SOURCE
ORGANISM
                        RESULT 9
AI459809/c
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86

EST 27-MAR-2003

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AUTHORS
TITLE
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KEYWORDS
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                      FEATURES
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                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab host="DH108"
/clone_lib="BARC SBOV"
/note="Vector: DCMV SBOWT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 CAAACAGIGGACCI---CAACGAAGGAGAIGCIGCACCIGAACCCACWGAAGCGAAACIC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 caaacacredarcredecgaagaagagagagagagacacaccegarccegagaagaagcacce 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 AAAAGAGAAAGCAAA---CCAAGAACCTCTCTGATGRCGTTTCTCAGACAAATG 588
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Bdlg. 200 Rm 2A, Belteville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 89.8; DB 2; 76.3%; Pred. No. 3.9e-15; iive 2; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
                                                                                                                                                                                                                 /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                  FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Flate: 132 row: N column: 19
Seq primer: ATTTACGGGACACATARG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG Plate: 3 row: B column: 3
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                                     and -minmatch 12 options.
PCR PRimers
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/mol_type="mRNA"
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/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="BARC_SBOV"
/clone_lib="BARC_SBOV"
/clone_lib="Roctor: pCMV SPORT6; Site_l: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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602831931F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4986798 5',
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NIH-MGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Llaminge.llnl.gov
High quality sequence stop: 668.
High quality sequence stop: 668.
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/note="Torgan: Colon; Vector: Torgan: Torgan: Colone Torgan:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 668)
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                                                                                                                                                                     /organism="Bos taurus"
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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AKO08957

Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416M21 product:weakly similar to BREAST CARCINOMA AMPLIFIED SEQUENCE I (NOVEL AMPLIFIED IN BREAST CANCER 1) (AMPLIFIED AND OVEREXPRESSED IN BREAST CANCER) [Homo sapiens], full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikaj,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer consequence analysis (RISA) system--384-format 20530913
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cONAs
Nature 420, 563-573 (2002)
268 AGGCAGGCCCACCTCACTACCGCTGGAAAGTTGTTTTGGAAGAAGTCAGTTAAGGAGG 327
                                                                                                                                                                                                                      452 AGTCCAAGGAAGTAGAATCAGCCTTACAAACAGTGGACCTCAACGAAGGAGGATGCTGCAC 511
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                      445 CTGAACCCACAGACGTAAAAGTCAAAGAAGAAAGAAAGCAAAACCCCGGAAGAAGACCCTCTGATGG
                                                                                                                                                        CTGAACCCACWGAAGCGAAACTCAAAAGAGAAAGAAAGCAAACCAAGAACCTCTCATGATGR
                                                                                                                                                                                                                                                                                 388 gécrrgágaagragaarccagcrracaakrgregarcrcagrea---agagacccagc
                                                                                              TTTTCTTATTACCTGGCAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High-efficiency full-length CDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
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/clone="IMAGE:6529081"
/lab_host="DH108 (TI phage-resistant)"
/clone=lib="WOI GGAP CO24"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                               332 AGGGGGGCAGCAAGGACCCCACTTTGTAAAACATGTTTTGGGGGAATGTTTTGTTTTCA 391
                                                                                                                                                                                                                          207 AGCCAGGCCCACCTCACTACCGCTGGGAAAGTTGTTTTGGAAGAAGACTCAGTTAAGGAGG 266
                                                                                                                                                                                                                                                                                           451
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                       392 TTTTCTTATTACCTGGCAAAATAATCCAGGTGGTGTGTGAGTCACCAGTAGAGATTATAA
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Pred. No. 4.4e-14;
2; Mismatches 96;
                                   Score 86.6; DB 4;
Pred. No. 4.1e-14;
2; Mismatches 96;
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/mol_type="mRNA"
/strain="FVB/N"
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Mus musculus
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BU841356.1 GI:24025792
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332 AGGGGGCAGCAAGGACCCCACTTTGTAAAACATGTTTTGGGGGAATGTTTTGTTTTCA 391

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SEGI PRSEESNVKDSSCQTSNSVEKTPSPPEPEPAGTAQKNKETSSSKDKKSVDKKSA
TENSKQKNGKQEVREPAPCVQPPTVEANAMQTGDKTPKKSEKRRQSLGGFLKGLGPKR
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GQKMSETQAKSKKKRLDSPRLGLSFRKLPRHKDTENSPTTSANLKSDKANFTPQETRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.jp/) for further
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEM), Laboratory for Genome Exploration Research (RIKEM) Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL.http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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clone_lib="RIKEN full-length enriched mouse cDNA library'
                    Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arawa, M., Hangagaki, T., Hara, A., Hayatau, N., Hiramoto, K., Hiramoto, T., Hiramoto, T., Hiramoto, T., Hiramoto, T., Hiramoto, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshission
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weakly similar to BREAST CARCINOMA AMPLIFIED SEQUENCE 1
(NOVEL AMPLIFIED IN BREAST CANCER 1) (AMPLIFIED AND
OVEREXPRESSED IN BREAST CANCER) [Homo sapiens]
(SWISSPROT [075363, evidence: FASTY, 56*ID, 70.3*length,
match=1371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome
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/detrain="c57BL/6"
/db_xref="FANTOM DB:2210416M21"
/db_xref="raxon:10090"
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12.0%; Score 86.6; DB 3; Length 2339;

Query Match

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 Pred. No. 5.8e-14;
2; Mismatches 96; Indels
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Job time : 3074.62 secs
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BC017656 Mus muscu
AC124012 Mus muscu
AC124231 Mus muscu
AC013555 Homo sapi
AC01555 Homo sapi
AC15605 Sequence
AC125105 Homo sapi
AC15160 Sequence
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AC25105 Homo sapi
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1 (bases 1 to 1288)
Gray, J., Collins, C., Hwang, S.-i., Godfrey, T., Kowbel, D. and
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Genes from the 20013 amplicon and their uses
Patent: US 5892010-A 5 06-APR-1999;
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ive 0; Mismatches
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/mol_type="unassigned DNA"
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5 from patent US 5892010.
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BX276189 Human DNA
AC051637 Homo sapi
CQ740312 Sequence
BC079550 Mus muscu
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BC079877 Mus muscu
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Maximum Match 100%
Listing first 45 summaries
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181 AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG

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CQ078477 Sequence BV014871 S212P6046 BC028776 Mus muscu

CQ069297 Sequence AF191309 Mus muscu BC058264 Mus muscu

CQ069297 AF191309 BC058264

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1288 1283.4 1265 11265 1137 1137 1137 1013 909.2 908.2 908.2 897.2 656.4

Result No.

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PAT 27-AUG-2002
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Patent: JP 2001524802-A 5 04-DEC-2001;
THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
OS Artificial Sequence
NO 3D 2001524802-A/5
PD 04-DEC-2001
PF 15-JUL-1996 US 08/680395,16-OCT-1996 US 08/731499 PR 15-JUL-1997 US 08/8532
PI JOB W GRAY, COLIN CONRAD COLLINS, SOO IN HWANG, TONY GODFREY,
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Gray,J.W., Collins,C.C., Hwang,S.I., Godfrey,T.,
Roumens,J.
      1288 bp DNA lir
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JOURNAL Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKEZ): Email s.wiemann@dKfz.heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.in the cDNA sequencing consortium of the German Genome (DKFZp686K2480) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcemzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the Clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/. FEATURES 11830 /organism="Homo sapiens" /mol type="MRNA" /db xref="texon:9606" /clone="DKFZp686K2480" /clone="DKFZp686K2480" /clone="DKFZp686K2480" /clone="DKFZp686K2480" /clone="DKFZp686K2480" /dev_stage="munan endometrium carcinoma cell line" /clone=[lb="686" (synonym: hlcc3). Vector pSportl_Sfi; host DNIONS site 1819	Query Match 99.6%; Score 1283.4; DB 9; Length 1830; Best Local Similarity 99.9%; Pred. No. 0; 1 Indels 0; Gaps 0; Matches 1284; Conservative 0; Mismatches 1; Indels 0; 0; Qy I GAGGCAGCAGAGAGAGACACCCCCCGCCCCGAGCCCTCTGAGCATCTGTGAGCATGGG 0 0 0 Db 300 GAGGCAGCAGCACCCCCCGCCCCGGCCCTGGAGCCCTCTGAGCATCTGTGAGCATGGG 359 0 Qy 121 TCCGTCTGGAACACCACGCCCCGGCCCTGGAGCCTTGAGCCTTGAGGCTGCTGAGGCCTTGAGGCTGCTGAGGCCTTGAGGCTGCTGAGGCCTTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCTGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCTGAGGCCTTGAGGCCTTGAGGGCGTGAGGGCTGAGGGCGTGAGGGCGTGAGGCGTGAGGGCGTGAGGGCGTGAGGGCGTGAGGGCGTGAGGGCGTGAGGGCGTGAGGGCGTGAGGGGCTAGGGGGCTAGGCGCTGAGGGCGCTAGGGGGCTAGGCGCTAGGCGCTGAGGGGGCTAGGGGGGGG	421 AAAGTCCTCCCCAAAGCCACCCCAAAGCCAGCTCCTCCTCCAGGGTCCCCCATG 720 AAAGTCTCCCCCAAAGCCACCCCCAAAGCCAGCTCCTCCTCCAGGGTCCCCCCATG 720 AAAGTCTCCCCCAAAGCCACCCCCAAAGCCAGCTCCTCCTCCTCCAGGGTCCCCCCCTG 721 AAAGAAATGGATGTCAGGGGTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 780 AAGCTGGAAATGGATGTCAGGGGTTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 780 AAAGAAAAGGCCGCAGTCCAACTGGAATCCTCAGTGAAGTCTCAACTTTGCAT 780 AAAGAAAAGGCCGCAGTCCAACTGGAATCCTCAGCATCTTCTAACTTTGCAT 601 TTTGCCTCGAGCCTCTTCCAGAGGCAAATACCTGCTGTTCTGATTCTACAAGCCCAG 701 TTTGCCTCGAGCCTCTTCCAGAGGCAAATACCTGCTGTTCTGATCTTGGGCCCAGGCCCAGTTTTGCCTCGAGCCCCAGTTTCTCAGAGCCCCAGTTTTCTCAGAGCCCCAGTTTTCTCAGAGCCCCAGTTTTTCCTTCTAGAGCCCAGTTTTTCTTTTTTTT
	ACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCGCTTG TCAGTGGACCAGCAAAGCAA	HSM808295 HSM808295 HSM808295 HSM808295 HSM808295 HSM808295 HOMO Sapiens MRNA; CDNA DKFZp686KZ480 (from clone DKFZp686KZ480). CESSION BX648148 BX648148.1 GI:34367307 WWORDS HOMO Sapiens (human) OKGANISM HOMO Sapiens (hordata; Craniata; Vertebrata; Buteleostom; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo. FRRENCE I (bases 1 to 1830) AUTHORS ANSORGE, W. Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and The German Human CDNA Consortium Title Direct Submission

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
             CAAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATCAGTCACTGG
                                                                  CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGGACAAAATTTCTGAAAAAACATG
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Patent: EP 1308459-A 373 07-MAY-2003;
Helix Research Institute (JP); Research
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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GNDTGTPBELETGPEGKGCFSYQNSPGSHLSNQDARNESLLSDASDQVSDIXSVCGRD

ASDKKAHTHYRLPNEAHNCHDKAAYANILSDSYWSGLGLGFKLSNSERRNCDTRNG

SNKSDFDWHQDALSKSLQQULSSRSVSKPSLEPSSVQLYRQSSKMCGTVFTGASRFRCR

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SDCTAASTTELKKESKKERPERTSKDERVYKSEDPLQNEDPTISYGVLREBLED
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IRPNIJNKLRPIAPTATAINKANGAPSWSYYPSIHAAYQLSGTIKRPLPMGSRVLG
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SENSEGDSPRKSETPPEAKKTELGPHEBEKLIKREGSSEKEKPQPLEPTSALSNGCAL
ANNAPALPCINPLASALGSVLANHLGKATEPLKSPGCSSPSSSTISWFHKSNIAWDKP
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VKVLPRATTPKPASSSRVPPWKLENDYRRFEDVSSSVSTIHKKRGROSNWNPOHLLIL
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RVSSAQRSPETIAAEBDTDSKFKCKLCCRTFVSKHAVKLHLSKTHSKSPEHHSQFYTD
                                                                                                                                                                                                       Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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                                                                                                         Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
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/clone Tib="CTONG2"
/note="cloning vector: pME18SFL3"
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   human cDNA sequencing project
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                                                                                                             3138 TCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGCTCTGCAGGACG 3197
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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PRI 25-FEB-2003

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em; EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at their worknessed from part of bacterial clone contigs of human chromesome 20, constructed by the Sanger Center Chromosome 20 mapping Group. Further information can be found at http://www.anger.ac.uk/HGP/Chr20

RPQ-678015 is from the library RPC14 constructed by the group of Pieter de Jong. Further information can be found at http://www.chori.org/bacpac/home.htm

VECTOR: POWNER PETOR: Further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 54161)

                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (25-FFB-2003) Wellcome Trust Sanger Institute, Hinxton, Submittedshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
BX276189

Human DNA sequence from clone RP4-678D15 on chromosome 20q13.13-13.2, complete sequence.
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iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
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/db_xref="taxon:9606"
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/clone="RP4-678D15"
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Best Local Similarity 100.
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                                                          AACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAGCAAGAAAGCCGAGTCCTCGCAA
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ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS	<u>. •</u>			·		TITLE	JOURNAL REFERENCE AUTHORS						TITLE JOURNAL COMMENT	•
40632 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCC 40691	181 AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG 240 	241 CGGGTCTTGAGTCCTGCCTCCACAAGGTCAGCCAGCGTGCCAGGGGCTACCTGTTTGAG 300	AACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAGCAAGAAAGCCGAGTCCTCGCAA	40812 AACAGCGATCGGCCCATTGACCTGACGAGAGCAGAAAGCAGAAAGCGGGGTCCTCGGAA 40871 361 GCACAATCTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTG	40872 GCACAATCTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTG	421 AAAGTCCTCCCCAAAGCCACCCCAAAGCCACCTCCTCCTCCAGGGTCCCCCCATG 480	481 AAGCTGGAAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 540	541 AARAGAARAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCAG 600	TTTGCCTCGAGCCTCTTCCAGACATCAGAGCAAATACCTGCTGTCTGATCTGGCCCCA	661 CAAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATCAGTCACTGG 720 	721 CTGGCCAACGTCAAGTACCAGCTTAGGAAACGGGGGGGGACAAATTTCTGAAAAACATG 780 	781 GACAAAGGCCACCCCATCTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCCTTCT 840 	841 ACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCGCTTG 900 	901 TCAGTGGACCAGCAAAGCAAGGTGGAGCAAGAGATCTCCCGGGGTATCGTCGGCTCAGAGG 960 	961 TCTCCAGAAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAAGTTGTGC 1020 	1021 TGTCGGACATTTGTGAGCAAACATGCGGTAAAACTCCACCTAAGCAAAACGCACAGGAAG 1080 	1081 TCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGATAGCTCTGCAGG 1137
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AC051637 172256 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 20 clone RP11-664G18 map 20, WORKING DRAFT SEQUENCE, 27 unordered pieces.

RESULT 7 AC051637/c LOCUS DEFINITION

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                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 155286 bases at least Q40 Consensus quality: 164921 bases at least Q40 Consensus quality: 164921 bases at least Q30 Insert size: 176000; agarose-fp Insert size: 176000; agarose-fp Quality coverage: 3.9 in Q20 bases; sum-of-contigs Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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Best Local Similarity 100.
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AUTHORS Gray,J.W., Collins,C., Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H. JOURNAL Unpublished REFERENCE (bases 1 to 57493) AUTHORS Ricke,D.O. TITLE Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System JOURNAL Unpublished		REFERENCE 4 (bases 1 to 57493) AUTHORS Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Rodeski, H., Subramanian, S. and Martin, C.H. TITLE Direct Submission JOURNAL Submitted (30-MAR-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157,	REFERENCE 5 (bases 1 to 57493) AUTHORS Ricke, D.O. TITLE Direct Submission JOURNAL Submission COMMENT Seminore submitted (20-JUN-1998) DOE Joint Genome Institute	DOE Joint S urce	/organizations organizations //organizations//organ	/alone="%35" /alone="LBNL H65" /note="LBNL H65" repeat_region complement (408. 1147)	repeat_region complement(436. 1598) /rpt_family="MIR" repeat_region 1911. 2091	repeat_region complement(2129) /rpt_family="L1" .2293) misc_feature complement (30573173)	7170	/rpf taming=Alu" misc_feature complement(58976677) /note="6RAIL 2 excellent exon, frame 2" misc_feature complement(7201	xce] xce] 18"	/rpt_family="MER3" repeat_region complement(1375114053) /rpt_family="Alu" repeat_region 1425714288	/rpt_type=tandem /rpt_unit="ac" /rpt_unit="ac" /rpt_family="MIR"
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Matches 1136; Conservative
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/mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 6.78-275; Matches 1013. Conservative 1. Mismatches 0. Indels 0. Gans 0.	1 GAGGCAGCAGAAAGAAAACCCCAGCCCCTGAGCCACATCTGCTTGAGCAATGGG 60		121 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTCTCCTGCTCC 180 2134 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCC 180 2134 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCC 219	181 AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGACAAG 24	241 CGGTCTTGAGTCCTGCCTCACAAGGTCAGCCAGGGGTGTCCAGGGGGTTTGAG 30 242 CGGTCTTGAGTCCTGCCTCCACAAGGTCAGCCAGGGGGTGTCAGGGGGTTTGAG 30 2254 CGGTCTTGAGTCTCACACACACACACAGGGGGTTCAGGGGGTTCAGGGGGTTCAGGGGGGTTCAGGGTTCAGGGGGTTCAGGGTTCAGGGGGTTCAGGGTTCAGGGGGTTCAGGGTTCAGGGTTCAGGCGGTTAGAGGTTCAGAGGTTCAGGGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTCAGGGTTTCAGGGTTTCAGGTTTCAGGTTTCAGGGTTTCAGGGTTTCAGGGTTTCAGGGTTTCAGGTTTCAGGTTTCAGGGTTTCAGG	301 AACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAGCAAGAAAGCCGAGTCCTCGCAA 3	361 GCACAATCTTGTATGTCCCCACCTCAAAGCACGCTCTGTCTG	421 AAGTCCTCCCCAAGCCACCCCAAAGCCAGCCTCTCTCCAGGGTCCCCCCATG 480 421 AAAGTCCTCCCCCAAGCCACCCCAAAGCCAGCCTCCTCCAGGGTCCCCCCCATG 480	481 AAGCTGGAAATGGATGTCAGGGGTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 481 AAGCTGGAAATGGATGTCAGGGGGTTTGAGATGTCTCCAGTGAAGTCTCAACTTTGCAT 2494 AAGCTGGAAATGGATGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGAGTTTAGAGTTAGAGTTAGAGTTAGAGTTTAGAGTTAGAGTTTAGAGTTTAGAGTTTAGAGTTTAGAGTTAGAGTTTAGAGTTTAGAGTTTAGAGTTAGA	541 AAAGAAAAGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCAG 6	601 TTTGCCTCGAGCCTCTTCCAGACATCAGAGGCAAATACCTGCTGTCTGATCTGGGCCCA 6	Oy 661 CAAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATCAGTCAG	Qy 721 CTGGCCAACGTCCAAGTTTGGAAAACGGGCGGGCACAAAATTTCTGAAAAACATG 780 	Qy 781 GACAAAGGCCACCCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCCTTCT 840	Qy 841 ACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCGCTTG 900	Oy 901 TCAGTGGACCAGCAAGCTGGAGCAAGAGATCTCCCGGGTATCGTCGGCTCAGAGG 960	Qy 961 TCTCCAGAAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAA 1013
Db 46106 GCACAATCTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTG	QY 421 AAAGTCCTCCCCAAAGCCACCACCACGCTCCTCCTCCAGGGTCCCCCCATG 480	Oy 481 AAGCIGGAAAIGGAIGTCACGCGCTTTGACGAIGTCTCCAGTGAAGTCTCAACTTTGCAI 540 bb 46226 - AAGCIGGAAAIGGAIGTCAGCGCTTTGAGGAIGTCTCCAGTGAAGTCTCAAGTTTGCAI 46285	OY 541 AAAAGAAAAGGCCGCAGACCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCAG 600	dy 601 TITGCCTCGAGCCTCTTCCAGACATCAGAGGCAAAAACCTGCTGTCTGATCTGGGCCCA 660 bb 46346 TITGCCTCGAGACCTCTTCCAGACATCAGAGGCAAATACCTGCTGTCTGATCT-GGCCA 4604	Qy 661 CAAGAGCGTATGCAAATCTCTAAGTTTACGGACTCTCAATGACCACTATCAGTCACTGG 720 Db 46405 CAAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATCAGTCACTGG 46464	OY 721 CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGGACAAAATTCTGAAAAACGTG 780 	Qy 781 GACAAAGGCCACCCATCTTTATTGCAGTCACTGTGCCTCCCAGTTCAGAACCCCTTCT 840 bb 46525 GACAAAAGGCCACCCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCCTTCT 46584	QY 841 ACCTACATCAGTCACCTGGGTTTCCAAATGAAGGACATGACCCGCTTG 900 L	QY 901 TCACTGGACCAGCAAAGCAAGCAAGAGATCTCCCGGGTATCGTCGGCGTCAGAGG 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 961 TCTCCAGAAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAAGTTGTGC 1020	OY 1021 TGTCGGACATTTGTGAGCAAACATGCGGTAAAACTCCACCTAAGCAAAACGCACAGGAAG 1080	Qy 1081 TCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGCTCTGCAGG 1137 Db 46825 TCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGCTCTGCAGG 46881		110N Sequence 10N CQ740312 N CQ740312. DS	_	REFERENCE 1 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses	Thereof JOURNAL Patent: WO 02068579-A 26246 06-SEP-2002; PE COrporation (NY) (US) FEATURES Location/Qualifiers	source 1.3168 /organism="Homo sapiens"

2974

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RESULT 10 BC079550 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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QSVLNNHLGKKTTEPLAREPSCSSPNSSTSPVFHKSSLHVVDKPVISFTSTRPAASVARH
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DVSDKKANTHPKLPSEPHNCMDKMTAVYANILSDSYWSGLGLGFKLSNSERRNCDTLV
ELTVHMNETGHYQDDNRKKDKLRPTSYSKPRRAFQDMDKEDAQKVLKCMFCGDSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LÓDLSVIHMIKTKHYOKVPLKEPVPTISSKMVTPAKKRVFDVNRPCSPDSTTGSLADSF
SOSKSANLOLPSNSRYGYQNGASYTMOFBACKSQILKCHSCGSSHDTLOQUTTHMVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENTVTTAINKAQNGAPSWSAYPSIHAAYQLSEGTKPPWAMGSQILQIRPNLANKLRP
IAPKWKGMPLGPVPTSLALYTQVKKETEDKDEVVKQCGKESPHEEATSFSQPEGESFS
KIEPPSESRKAEPCPLKEEEKPQKEKPEPLEPVSSLTNGCAPANHTPALPSINPLSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1830 AGAAAGAGAAACCGGAGCCCTTAGAACCAGTATCTTCTCTGACCAATGGCTGTGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1890 CTAACCACCCCGGCTCTGCCTTCCATCAACCCGCTCAGTGCCCTGCAGTCCGTCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1950 ACAACCACCTGGGCAAAGCCCACGGAGCCCTTGCGCTTCCTGCTCCAGTCCCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAGCCGGTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2010 caadcacaaagcccccgrgrrccaraaarccagccrccacgrgrggagagagccggrcaraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 GTCCTGCCTCCACAAG---GTCAGCCAGCGTGTCCAGGCGCTACCTGTTTGAGAACAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2070 greceaecriceáceágecagacagacagacagacagacacracracragarragadadas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 CTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTGACATCGCCGACATGGTCAAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 TCCCCAAAAGCCACCACCCCAAAGCCAGCCTCCTCCTCCAGGGTCCCCCCCATGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2250 TCCCCAAAGCCACCCCCAAAGCCAGCCGCCTCCTCCTCGAGGGTCCCTCTATGAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 AAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCATAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCCAGCCCCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AGAAGGAGAAACCCCCAGCCCCTGGAGCCCACATCTGCTCTGAGCAATGGGTGCGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 4902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.6%; Score 909.2; DB 10;
Best Local Similarity 88.4%; Pred. No. 1.6e-245;
Matches 999; Conservative 0; Mismatches 128;
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                                                                                                                                                                      /clone_lib="NIH_E
/lab_host="DH10B"
                                                                                                                                                                                                                                                  .2950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Couract: most mesh uses.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.4G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gailthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hhgri.nih.gov/
Contact: nisc_mgc@hhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin.B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., (Guna,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 176 Row: i Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
1. 4902
                                                                                                                                                  BC079550 4902 bp mRNA linear ROD 03-AUG-2004 Mus musculus cDNA clone MGC:90763 IMAGE:6852953, complete cds. BC079550
                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-MG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                        BC079550.1 GI:50926038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 4902)
Director MGC Project.
                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 4902)
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PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

JOURNAL

TITLE

1889

20

Gaps 3, 1949

190

130

2009

250

2069

307

2129

367

2189

2249

427

487

2309

547

Bource

FEATURES

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variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projectsf/C_elegans/wormpep RP23-105H6 is from the RPCI-23 Mouse PAC Library de Jong.

For further details see http://www.chori.org/bacpac/home.htm 13388 13448 13508 13208 13209 CAAGCACAAGCCCCGTGTTCCATAAATCCAGCCTCCACGTGGTGGACAAGCCGGTCATAA 13268 13269 GTCCCACCTCCACCAGGCCGGCGGCCAGCGTGGCCAGACACTACCTGTTTGAGAAACACG 13328 1, 190 130 250 367 487 547 427 607 2 13449 TCCCCAAAGCCACCCCCAAAGCCAGCCGCCTCCTCGAGGGTCCCTCCTATGAAGCTGG 131 ACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCCAGCTT 13389 ccrecacereceaecreaedadeargeargerererereaearrecreararegree AAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCCAACTTTGCATAAAAGAA 11 AGAAGGAGAAACCCCCAGCCCCTGGAGCCCCACATCTGCTCTGAGCAATGGGTGCGCCCTCG CCAACCAGGCCCGGCCCTGCCATGCATCAACCCACTCAGCGCCCTGCAGTCCGTCTGA 13149 ACAACCACCTGGGCAAAGCCACGGAGCCCTTGCGCTTCCCTGCTCCAGTCCCAACT CAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAGCCGGTCTTGA GTCCTGCCTCCACAAG---GTCAGCCAGCGTGTCCAGGCGCTACCTGTTTGAGAACAGCG ATCAGCCCATTGACCTGACCAAGTCCAAAAGCAAGAAAGCCGAGTCCTCGCAAGCACAAT CTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTGACATCGCCGACATGGTCAAAGTCC TCCCCAAAGCCACCCCCAAAGCCAGCCTCCTCCTCCAGGGTCCCCCCCATGAAGCTGG 548 AAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCAGTTTGCCT Gaps Length 218037; Indels 70.6%; Score 909.2; DB 10; 88.4%; Pred. No. 2.6e-245; ive 0; Mismatches 128;

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SRSQPEGESFSKIEPPSSRKAEPCPLKEEEKPQKEKPPFLESKLYVDKPVISFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: Plate: Row: Column: 0 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRPAASVAHHYLFERYTDQFIDLTKSKSKRAESSQAGSCTSPPQKHALCDIADMYKVL
PKATTPKPAASSRVPPMKLEIDVRRFEDVSSEVSTLHKRKGRQSWNRPQHLLILQAQF
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AQRSPETIAGEEDTDSKFKCKLCRRTFVSKHAVKLHLSKTHSKSPEHHSQFVADVDEE
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SSNDTGTDEELETGPEQKGYFSCQNSPGSHLSNQDAENESLLSDASDQVSDVKSVCGR
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                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lih, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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Web Site: http://genome.uiowa.edu
Contact: bento:soaresGulowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Stshler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                               Direct Submission
Submitted (09-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2410 AGAAAGAGAAACCGGAGCCCTTAGAACCAGTATCTTCTCTGACCAATGGCTGTGCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    э,
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protein id="AAH79877.1"
db_xref="GI:51260243"
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                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Director MGC Project.
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 4041)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Wainy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Halton, E., Ketteman, W., Madan, A., Rodrigues, S.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and mouse cDNA sequences

N. Droc. Wall. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

E. (bases 1 to 4041)
                                                                                                                                                                                                                                                                                                                                                                    13749 ACGTCAAATACCAGCTTAGGAAACAGGTGGGACAAAGTTCCTGAAAAACATGGACAAAG
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                                                                               CGAGCCTCTTCCAGACCTCTGAGAGGGCAAATACCTGCTTTCTGACCTGGGCCCCCAAGAGC
                                                                                                                                                                                                            GGATGCAAATCTCCCAAGTTCACCGGACTCTCCATGACCACAATCAGCCACTGGCTG
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ROD 17-APR-2000

us-08-731-499-5.rge

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NGCAPANHTPALPŠINPLSALQSVLNNHLGKATEPLRSPSCSSPNSSTSPVFHKSSLH
VVDKPVISPTSTRPAASVARHYLFENTDQPIDLTKSKSKRAESSQAQSCTSPPQKHAL
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                                                                                                                                                                           Caubit, X., Core, N., Boned, A., Kerridge, S., Djaball, M. and Fasano, L. Vertebrate orthologues of the Drosophila region-specific patterning
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PMAMGSQILQIRPNLANKLRPIAPKWKGMPLGPVPTSLALYTQVKKETEBRDEVVKQC
GKESPHEEATSFSQPEGESFSKIEPPSESRKAEPCPLKEEEKPQKEKPFPLEPVSSLT
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VEQEISRVSSAQRSPETIAGEEDTDSKFKCKLCRRTFVSKHAVKLHLSKAHSKSPEHH
SQEVADVDEE"
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                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="zinc finger protein, mtsh2; related to drosophila region specific patterning gene teashirt; contains 3 teashirt-like zinc finger domains (Cx2Cx12HMx4H) and 2 other zinc finger domains (Cx2Cx12HX3-4H) and 2
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Coubit,X., Core,N., Boned,A., Djabali,M., Kerridge,S. and Direct Submission
Submitted (23-NOV-1999) LGPD, CNRS Case907, Parc Scientifi
                  bNA linear gene, partial cds.
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/gene="T8h2"
/note="putative; Region: homeodomain"
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88.3%; Pred. No. 3.9e-242;
ive 0; Mismatches 128;
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
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Mus musculus teashirt 2 (Tsh2) g
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20171079
                                                                                                 Mus musculus (house mouse)
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/gene="Tsh2"
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CQ078477 LOCUS LOCUS LOCUS DEFINITION Sequence 14277 from Patent W00157278. ACCESSION CQ078477.1 GI:41048346 KEYWORDS CQ078477.1 GI:41048346 KEYWORDS CQ078477.1 GI:41048346 KEYWORDS CQ078477.1 GI:41048346 CQ078477.1 GI:41048346 Homo sapiens (human) ORGANISM Homo sapiens (human) REPERBUCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells JOURNAL Patent: W0 0157278-A 14277 09-AUG-2001; FEATURES LOCATION HUMAN Acomica, Inc. (US) LOCATION HUMAN BOLOGE LOCATION HUMAN LOCATION HUMAN ACOMICA LOCATION HUMAN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="MAP ACO04505.1~EXPRESSED IN HELA, SIGNAL = 1~N HIT: AF207880.1, EVALUE 0.00e+00~EST HUMAN HIT: H12950.1 EVALUE 0.00e+00~SWISSPROT HIT: P22265, EVALUE 1.00e-07" atch 51.0%; Score 656.4; DB 6; Length 2012; cal Similarity 99.8%; Pred. No. 4.7e-174;	VALIVE 0; MISMACCHES GAGAAGGAAACCCCAGCCCTGGAGC	QY 61 TGCGCCCTCGCCAACCACGCCCTGCCATGCATGCACCACTCAGGGCCCTGCAG 120	Qy 121 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCCTCCTGCTCC 180	QY 181 AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG 240	QY 241 CCGGTCTTGAGTCCTGCCTCCACAAGGTCAGCCAGCGTGTCCAGGGGCTACCTGTTTGAG 300	OY 301 AACAGGGATCAGCCCATTGACCTGACCAAGAGCAAGAAAGCCGAGTCCTCGCAA 360	OY 361 GCACAATCTTGTATGTCCCCACCTCAGAAGCACGCTCTGTCTG	QY 421 AAAGTCCTCCCCAAAGCCACCACCAAAGCCAGCCTCCTCCTCGAGGTCCCCCCATG 480	Qy 481 AAGCTGGAAATGGATGTCAGGGGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 540	QY 541 AAAAGAAAAGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCAG 600	Qy 601 TITGCCTCGAGCCTCTTCCAGACATCAGAGGCAAATACCTGCTGTGTCTGGGCC 658
Db 2237 CTAACCACCCGGGTCTGCACCGGTCAGTGCCTGCAGTCCGTGA 2296 131 ACAATCACTTGGGCAAAGCCACCGGTCAGTGCCCTGCAGTCCGTCC	Oy 368 CTIGTATGTCCCACCTCAGAAGCACGCTCTGACATCGCCGACATGGTCAAAGTCC 427 Db 2537 CCTGCACGTCCCCACCTCAGAAGCATGCTCTGTGTCAATATGGTCAAAGGTCC 2596 Qy 428 TCCCCAAAGCCACCCCCAGAAGCTCCTCTCTCCTCCAGGGTCCCCCCCATGAAGCTGG 487 Db 2597 TCCCCAAAGCCACCCCCAAAGCCAGCCTCCTCCAGAGGTCCCTCTATGAAGCTGG 2656 Qy 488 AAATGGATGTCAGGGGTCTCTCCAGTGAAGTCTCCAACTTTGCATAAAAGAA 547		OY 608 CGAGCCTCTTCCAGACATCAGAGGGCAAATACCTGCTGTCTGATCTGGGCCCACAAGAGC 667	OY 668 GTATGCAAATCTCTAAGTTTACGGACTCTCAATGACCACTATCAGTCACTGGCTGG	OY 728 ACGTCAAGTACCAGCTTAGGAAAACGGGGGGACAAAATTTCTGAAAACATGGACAAAG 787	OY 788 GCCACCCCATCTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCCTTCTACCTAC	OY 848 TCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCGCTTGTCAGTGG 907	QY 908 ACCAGCAAAGCAAGGAGGAAGCAAGAATCTCCCGGGTATCGTCGGCTCAGAGGTCTCCAG 967 Db 3077 ACCAGCAAAGCAAGGAGGAGATCTCCCGAGTGTCGTCGGCTCAAAGGTCTCCAG 3136	DY 968 AAACAATAGCTGCCGAAGAGGACACAGAGACTCTAAATTCAAGTGTAAGTTGTGCTGTGGA 1027 DD 3137 AAACAATAGCTGGCGAAGAGACACAGAGACTCTAAATTCAAGTGTAAGTTATGCCGTCGGA 3196	Qy 1028 CATTIGTGAGCAAACATGCGGTAAAACTCCACCTAAGCAAAAGGCACAGCAAGTCACCG 1087	OY 1088 AACACCATTCACAGTTTGTAACAGACGTGGATGAAGAA 1125	RESULT 14

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Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
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S212P60463FH5.TO CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
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Whitehead Institute for Biomedical Research, Center for Genome
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/strain="c2ECHI/Es"
/db_rxef="teaxon:1009"
/map="+ 2 22-621 170891742-170892341"
/clone_lib="CZECHII/Es"
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/organism="Mus musculus"
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Email: kersli@genome.wi.mit.edu
Primer A: None
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Mus musculus
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Tel: 6172521477
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Listing first 45 summaries
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ALIGNMENTS

BP

AAV04700 standard; cDNA; 1288

RESULT 1 AAV04700 AAV04700;

20q13 amplicon; chromosome 20; tumour; detection; homeobox T shirt; chromosomal abnormalities; probe; gene therapy; antisense inhibition; treatment; age-related macular degeneration; retinitis pigmentation; Leber's congenital amaurosis; ds. Rommens J; Kowbel D, Godfrey T, Homo sapiens 20q13 amplicon 41.1 transcript. Gray JW, Collins CC, Hwang S, 96US-00680395. 96US-00731499. 97US-00785532. 97WO-US012343. (first entry) (REGC) UNIV CALIFORNIA. WPI; 1998-110587/10. Homo sapiens. 15-JUL-1996; 16-OCT-1996; 17-JAN-1997; 21-JUL-1998 WO9802539-A1 15-JUL-1997; 22-JAN-1998.

New sequences from the 20q13 amplicon - used for detecting chromosomal abnormalities, particularly tumours, and for developing products for treating diseases.

Claim 1; Page 62; 91pp; English.

The sequence is that of a cDNA sequence 41.1, which was isolated from the 20q13 amplicon. It shows homology to the homeobox T shirt gene in Drosophila. It can be used as a probe for the detection of chromosomal abnormalities at 20q13. It and other sequences isolated from the 20q13

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Emerling BM, Forsythe IJ, Gietzen KJ;
Hafalia AJA, Honchell CD, Ison CH, K
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Griffin JA,
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                  are useful as probes or as probe targets for monitoring the relative copy number of corresponding sequences from a biological sample such as tumour cells. The sequences can also be used in therapeutic applications for modulating the expression of the endogenous gene or the activity of the gene product. Examples of the rapeutic approaches include antisense inhibition of gene expression, gene therapy, and monoclonal antibodies that specifically bind the gene products. The products can also be used in the treatment of other diseases, e.g. age-related macular degeneration, Leber's congenital amaurosis and retinitis pigmentation
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Matches 1288; Conservative 0; Mismatches 0; Indels 0;
amplicon are consistently amplified in primary tumours. These
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                                                            CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGGACAAAATTTCTGAAAAACATG
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/product= "Clone CTONG20074000 protein"
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                                                                                                                                                                                                                                                                         ABZ79873 to ABZ79905 encode the human nucleic-acid associated proteins designated NAAP-1 to NAAP-33 given in ABP96218 to ABP96250. The NAAP sequences have cardiant, cytostatic and neuroprotective activities, and can be used in gene therapy. The NAAP sequences can be used for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional NAAP e.g. cardiovascular or neurological disorders or cancer
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    Lehr-Mason PM;
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                                                                                                                                                         New human nucleic acid-associated proteins polypeptide, useful for preparing a composition for diagnosing or treating e.g., cardiovascular or neurological disorders.
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  S, Lee SY, Li JX, Lu DAM, Lu Y, Lehr-Ma
, Sprague WW, Tang YT, Thangavelu K;
Walia NK, Warren BA, Xu Y, Yao MG, Yue
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ative 0; Mismatches
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    Lal PG, Lee BA, Lee S,
Nguyen DB, Ramkumar J,
Thornton M, Tran UK, Wa
Yue H, Zebarjadian Y;
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P-PSDB; ABP96228.
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                                                                                                                                                                                                                                                                                                 The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, immunologically assaying the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide in an expressible manner and an antisense polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of genes may be included in their assured in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, creameription-related proteins, disease-related proteins and genes encoding them can be used as indicacrs for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate encoding them can be used as indicacrs for diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office.
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                                                                                 Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCGCCCTCGCCAACCACGCCCCGGCCCTGCCATGCATCAACCCACTCAGCGCCCTGCAG 120
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Matches 1265; Conservative 0; Mismatches
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                               (HELL-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                        Claim 1; Page; 222pp; English
25-JAN-2002; 2002US-00350978
                                                                                                                                                                                                                                        targets of gene therapy.
                                                                               Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                    WPI; 2003-450961/43.
P-PSDB; ADB64189.
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Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; meuroprotective; antiamemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 20; gene; ss.

Homo sapiens.

WO2003029271-A2

10-APR-2003

24-SEP-2002; 2002WO-US030474

24-SEP-2001; 2001US-0324631P

(HYSE-) HYSEQ INC

Wehrman T; Weng G; Wang J, Wang Z, Ren F, Xue AJ, Zhao QA, Wang D, Ma Y, Asundi V, Tang TY, Zhang J, Ren r,
Zhou P, Ghosh M, Wang D, Ma

WPI; 2003-371981/35. P-PSDB; ADC30994.

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 105; 1185pp; English

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the crecombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of convention further discloses methods for a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention capturession or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the captain of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 3442 BP; 1006 A; 949 C; 858 G; 629 T; 0 U; 0 Other;

78.7%; Score 1013.6; DB 10; Length 3442; 97.3%; Pred. No. 1.6e-286;

Best Local Similarity

Query Match

3313 ragrirccacrirccaccrosarcccrcacacrigaacc 3352

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 Human, immunosuppressive, antiarthritic, ss, antirheumatic, cytostatic, cardiant; vasotropic, cerebroprotective, nootropic, neuroprotective; antibacterial, virucide, fungicide, opthalmalogical; vulnerary; secreted protein; rhematoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; nervous system disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin againg; food additive; preservative; antiproliferative.
                                                                                                                 Human cDNA encoding a novel secreted protein, Seq ID 628,
                                              AAS26449 standard; cDNA; 2449 BP
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24-FEB-2000; 2000US-0180628P.

22-FEB-2000; 2000US-01864664P.

22-MAR-2000; 2000US-018974P.

16-MAR-2000; 2000US-018974P.

19-MAY-2000; 2000US-01998123P.

19-MAY-2000; 2000US-020515P.

07-JUN-2000; 2000US-020515P.

07-JUL-2000; 2000US-0214886P.

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215 AAATACCTGCTGTCTGATCTGGGCCCACAAGAGCGTATGCAAATCTCTAAGTTTAAGGA
                                                                        GGCGGGACAAAATTTCTGAAAACATGGACAAAGGCCACCCCATCTTTTATTGCAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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2000US-0249300P.
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P-PSDB; AAU16462.
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14-JUL-2000; 2000US-0220964P.
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P-PSDB; ABU55530.
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BARASH S C.
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular orenal disorders.

The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointeetinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's a momaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and

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leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention
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  Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithalial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
 novel secreted protein, Seq ID 193
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
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19-MAY-2000;
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14-AUG-2000;
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 Human
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873 371 933 431

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CTCCACCTAAGCAAAACGCACAGCAAGTCACCCGAACACCATTCACAGTTTGTAACAGAC 1113
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                                                                                                                                                                                                                    GACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTGAGCAAACATGCGGTAAAA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene, ds; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antifilammatory;
                                                                                                                                                                                                                                                                                                                                                                                                    Griggarigaagaaragcricrigcaggacgaargccriragrirricccrirriccaggcric 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCACACACTGAACCCTTCTTCGTTGCACCATCCTGCTTCTGACATTGAACTCATTGAACT
                                                                      TTCCAAATGAAGGACATGACCCGCTTGTCAGTGGACCAGCAAAGCAAGGTGGAGCAAGAG
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                  TGTGCCTCCCAGTTCAGAACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGT
                                                                                            ATCTCCCGGGTATCGTCGGCTCAGAGGTCTCCAGAAACAATAGCTGCCGAAGAGGACACA
                                                                                                                                                                GACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTGAGCAACATGCGGTAAAA
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TGTGCCTCCCAGTTCAGAACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGT
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2000US-0214886P.
2000US-0216647P.
2000US-0216880P.
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2000US-0224519P.
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2000US-0225268P.
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(ELISA). Disorders which are diagnosed or treated include autoimmune
diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

(ELISA). Disorders which are diagnosed or treated include autoimmune
classases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
cr errous system disorders e.g. Alzheimer's disease, infections caused by
carteria, viruses and fungi and ocular disorders e.g. corneal infection,
can also be used to aid wound healing and epithelial cell proliferation,
cr on also be used to aid wound healing and epithelial cell proliferation,
cr oprevent skin aging due to sunburn, to maintain organs before
cr esquerate tissues and in chemctaxis. The polypeptides can also be used
cas a food additive or preservative to increase or decrease storage
capabilities, fat content, lipid, protein, carbohydrate, vitamins,
cminerals, cofactors and other nutritional components. The present
c sequence encodes a novel secreted protein of the invention. Note: The
sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological sondition with the disorders and in diagnostic alleviating symptoms associated with the disorders and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573
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                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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Pred. No. 2.2e-215;
0; Mismatches 1;
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                                                                                                                                                                                                                                        Barash SC, Ruben SM,
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-02519869P.
08-DEC-2000; 2000US-025199P.
                                                                                                                                                                05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 99.9%;
Matches 771; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and tiple sclerosis), polyps and sinusitis), reproductive disorders, gastrointestinal disorders pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, bastein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and estage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular c
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2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
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2000US-0236369P.
2000US-0236802P.
2000US-0237037P.
2000US-0237038P.
2000US-0237039P.
2000US-0237040P.
2000US-0237040P.
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2000US-0229345P.
2000US-0229509P.
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2000US-0236327P.
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2000US-0241785P.
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RUBEN S M.
BARASH S C.
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                                                                      30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                         02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
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                                           14-AUG-2000;
22-AUG-2000;
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(RUBE/) F
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1173

611

1053

551

1233

731

09-AUG-2001.

Score 770.4; DB 8; Length 799; Pred. No. 2.2e-215;

59.8%; 99.9%;

Query Match Best Local Similarity

9

658

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1827 AAGCTGGAAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCAT 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                           1947 TTTGCCTCGAGGCTCTTCCAGACATCAGAGGCAAATACCTGCTGTGTCTGATCTGGCCC 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #5097 for gene expression analysis in human cervical cell sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                 TITGCCTCGAGCCTCTTCCAGACATCAGAGGCCAAATACCTGCTGTCTGATCTGGGCC
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100.0%; Pred. No. 6.5e-142;
iive 0; Mismatches 0;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0063266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
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Matches 521; Conservative
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expression in human cervical epithelial cells.
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                                                                                                26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0236359P.
                               30-JAN-2001; 2001WO-US000670
                                                                             2000US-0180312P
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Matches 657; Conservative
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                                                                    AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG
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28-JUN-2000;
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The present invention provides the protein and coding sequences of a number of ovarian and breast antigens. These are shown in AA/62467-AA/62572 and AA/42240-AA/42345. The sequences can be used in the diagnosis, prevention and treatment of breast and ovarian cancers, and their metastases. The present sequence is a genomic sequence of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directlinem WIPO at ftp.wipo.int/pub/published_pot_sequences
New isolated nucleic acids and polypeptides, useful for diagnosing treating and/or preventing human diseases and disorders.
                                                                                                                                                                                   Disclosure; SEQ ID NO 288; 520pp + Sequence Listing; English
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                                                                                       Score 390.4; DB 4;
Pred. No. 2.1e-103;
0; Mismatches 381;
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Local Similarity 62.4%;
les 673; Conservative
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GCCCTGCAGTCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCT
                                                                                                                                                                              CTGTTTGAGAACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAAGCAAGAAAGCCGAG
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                                                         TCCTGCTCCAGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTC
                                                                                                                   1072 CACAGCAAGTCACCCGAACACCCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGC
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 Human, reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           AACAAAACTCTGGGCCCACTGGGGCCACCGAGGAAGACTTGGGCTCCACATTCCAATGT 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCTCTGCAACCGGACTTTTGCGAGCAGCACGCAGTCAAACTGCACCTTAGTAAGACC 2238
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                                                           771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGCAAGTCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency;
                                                                                     ACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATG
                                                                                                                                                                                                                                                                                         ACCCGCTTGTCAGTGGACCAGCAAGGTGGAGCAAGAGATCTCCCGGGTATCGTCG
                                                                                                                                       AAAAACATGGACAAAGGCCACCCCATCTTTATTGCAGTGACTGTGCCTCCCAGTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA for novel secreted protein, SEQ ID 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 210-211; 339pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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Gulukota K, Graham JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         652 CTGGGCCCACAAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATC 711
                                                                                                                                                                                                                                                                                                 nucleic acid molecule encoding a reproductive system antigen is
                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 ACTITGCATAAAAGAAAAAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGAITCTA
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                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 9420; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 390.4; DB 4; Length 3604; Pred. No. 2.1e-103; 0; Mismatches 381; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1303 GCTTTGCAGTCCATCATGAACACCCACCTGGGCAAGGTGTCCAAGCCCGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3604 BP; 1002 A; 955 C; 853 G; 793 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                   used in preventing, treating or ameliorating a medical
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   06-DEC-2000; 2000US-0251479P.

08-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251866P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251989P.

11-DEC-2000; 2000US-025199P.

05-JAN-2001; 2001US-025199P.
                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                     Ruben
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Best Local Similarity 62.4%;
Matches 673; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention
                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                         WPI; 2001-465570/50
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The invention relates to a DNA which encodes a novel polypeptide. A vector containing the DNA is useful as a reagent in estimation of standard substance. The antibody is useful for detecting the vector containing the DNA and for screening substances and compounds that interact specifically with the vector containing the DNA. The vector containing the DNA is used as a pharmaceutical, in treatment or as preventive agent with respect to disease e.g., brain diseases preferably mental disorders. The present sequence represents human DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7081 BP; 1789 A; 1895 C; 1756 G; 1641 T; 0 U; 0 Other;
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          The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins encoded by the polynucleotides of the proteins or the expression of the polynucleotide. The polynucleotide can be used as probes for the identification and isolation of full length contains and genomic DNN. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders such as viral infections, becterial infections, fungal infections, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Albeimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. themophilia), inflammatory disorders (e.g. Crohn's disease) and in the treatment of burns, inclsions and ulcers. The proteins are also useful for regallating hematopoises, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              30.3%; Score 390.4; DB 6; 62.4%; Pred. No. 2.2e-103;
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3064 Adccacrederedecedareredadraceaerrededadededededededadedadrecera 3123
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                                                                                                                                                                                                             ACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATG
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                                                                                                                                        3124 AAGAACCTGGACACAGGGCATCCTGTTTTCTTTTGCAACGATTGTGCCTCTCAGTTCAGA
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                                                                    AAAAACATGGACAAAGGCCACCCCATCTTTATTGCAGTGACTGTGCCTCCCAGTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA encoding a novel polypeptide #40
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P-PSDB; ADF55476.
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                                                                                                                                                                                                                                                                                 -----AGTCCCTCGCTGGACCCGCTGGCGATGCTGTACAAGATCAGCAACAGCATG 4887
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                                       24;
  Length 7081;
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                                       Indels
Score 390.4; DB 10;
Pred. No. 3e-103;
                                       0; Mismatches 381;
30.3%;
62.4%;
                                       Matches 673; Conservative
                    Similarity
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                                    5722 CACGGCAAGTCTCCCCGAGGACCACCTGATCTATGTGACTGAGTTGGAGAAAACAGTAGC
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ADC31952 standard; cDNA; 1079

ADC31952;

18-DEC-2003

Human novel cDNA contig sequence, SEQ ID NO:2034.

biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosais; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 20; ss.

sapiens. Homo WO2003029271-A2.

10-APR-2003.

24-SEP-2002; 2002WO-US030474.

24-SEP-2001; 2001US-0324631P.

(HYSE-) HYSEQ INC.

Wehrman T; Weng G; Ren F, Xue AJ, Zhao QA, Wang J, Wang D, Ma Y, Asundi V, Wang Z, Drmanac RT; Zhang J, Haley-Vicente D, Ghosh Tang TY,

WPI; 2003-371981/35. P-PSDB; ADC32719 New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Example 2; SEQ ID NO 2034; 1185pp; English.

ADC30899 and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or amelicating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the industating and/or monoclonal antibodies for carrying out the methods that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the CDNA sequences of the invention (ADC31861-ADC328627) and the polypeptides encoded by the contigs (ADC332628 ADC33284). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet The invention relates to 971 novel human cDNA sequences (ADC29919-

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disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The mucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at five but wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                            676
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Matches 390; Conservative
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Search completed: May 5, 2005, 00:37:17 Job time : 901.572 secs This Page Blank (uspto)

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/note= "cDNA clone 41.1 with homology to homeobox T shirt gene from Drosophila"
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COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-ULL-1996
CLASSIFICATION NUMBER: US/08/680,395
FILING DATE: 15-ULL-1996
CLASSIFICATION NUMBER: US/08/680,395
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 023070-068900US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..1288
OTHER INFORMATION:
OTHER INFORMATION:
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Sequence 1, Appli
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Sequence 13, Appli
Sequence 173, App
Sequence 115513,
Sequence 11526,
Sequence 11526,
Sequence 11526,
Sequence 11509,
Sequence 11619,
Sequence 11619,
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Sequence 11611,
Sequence 14913, A
Sequence 14919, A
                                                                                            May 4, 2005, 23:46:20 ; Search time 289.356 Seconds (without alignments) 7283.499 Million cell updates/sec
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                                                                                                                                                              US-08-731-499-5
1288
1 GAGGCCAGCGAGAAAAAAAAAAAAAAAAATTC 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

cgn2_6/ptodata/1/ina/5B_COMB.seq:*

cgn2_6/ptodata/1/ina/6A_COMB.seq:*

cgn2_6/ptodata/1/ina/6B_COMB.seq:*

cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-625-5

US-09-510-543-21

US-08-828-008-1

US-09-023-655-773

US-09-049-016-11553

US-09-949-016-11553

US-09-949-016-11553

US-09-949-016-115595

US-09-949-016-1155905

US-09-949-016-115812

US-09-949-016-115998

US-09-949-016-116091

US-09-949-016-116184

US-09-949-016-116184

US-09-949-016-116184

US-09-949-016-116177

US-09-949-016-114915

US-09-949-016-114915

US-09-949-016-114918

US-09-949-016-114918
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Maximum Match 100%
Listing first 45 summaries
                                                                  - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 15639, A Sequence 3663, Ap Sequence 1177, Ap Sequence 12439, A Sequence 2711, Ap Sequence 2711, Ap Sequence 1127, Ap Sequence 1127, Ap Sequence 16722, A Sequence 5545, Ap Sequence 16722, A Sequence 16822, A Sequence 15822, A Sequence 15822, A Sequence 15822, A Sequence 14712, A Sequence 15822, A Sequence 16712, A Sequence 16722, A Sequence 16722, A Sequence 16822, A Sequence 16824, A Sequence 16824, A Sequence 16824, A Sequence 16824, A
                                                                             Sequence Seq
   US-09-621-976-15639
US-09-902-540-3663
US-09-949-016-12439
US-09-621-976-8976
US-09-201-132-94
US-09-902-540-1711
US-09-902-540-1127
US-09-949-016-15989
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                                              TCACCCGAACACCCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGCTCTGCAGGACG
                                                                                                                                 1141 AATGCCTTAGTTTCCACTTTCCAGCCTGGATCCCCTCACACTGAACCCTTCTTCGTTGCA
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APPLICANT: Gray, Joe W
APPLICANT: Collins, Collin
APPLICANT: Godfrey, Collin
APPLICANT: Godfrey, Tony
APPLICANT: Rowel, David
APPLICANT: Rowel, 100,000,000
FILE REFERENCE: 2500.124US3
CURRENT FILING DATE: 1997-07-15
EARLIER APPLICATION NUMBER: 08/785,532
EARLIER FILING DATE: 1997-01-17
EARLIER PILING DATE: 1996-10-16
EARLIER PILING DATE: 1996-10-16
EARLIER PILING DATE: 1996-10-16
EARLIER PILING DATE: 1996-10-16
EARLIER PILING DATE: 1996-07-15
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US-08-892-695-5
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100.0%; Score 1288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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38; Conservative
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Patent No. 6517837

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.

APPLICANT: Scanlan, Matthew J.

APPLICANT: Chen, Yao-Tseng

APPLICANT: Chen,
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                                                                                                                                                                                                                                                                                      540 TAAAAGAAAAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCA
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Patent No. 593316
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Criemer, Nelson, B.
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 Length 1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080 GTCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGC
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                                                                                                                                                             Score 256.4; DB 2;
Pred. No. 5.8e-71;
0; Mismatches 206;
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STREET: 1155 Avenue of the Americas
                                                                                                                                                               Query Match
Best Local Similarity 67.2%;
Matches 437; Conservative
LOCATION: 1...282
OTHER INFORMATION:
NAME/KEY: FSh 22
LOCATION: 1...1144
OTHER INFORMATION:
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STATE: NY
COUNTRY:
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US-08-828-008-3
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                                                                                                                                                                                       2188 ACTGCTTCTACATACATAAGTCATTTGGAGACACACTTGGGCTTCAGCCTGAAGGATCTC 2247
                                                                                                                                                                                                                                                                               2248 TCCAAGCTGCCACT---CAATCAGATTCAAGAACAGCAGAATGTTTCGAAAGTCCTCACC 2304
                                                                                                                                                                                                                                                                                                                                                        2305 AACAAAACTCTGGGCCCACTGGGGGCCACCGAGGAAGACTTGGGCTCCACATTCCAATGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2365 AAGCTCTGCAACCGGACTTTTGCGAAGCAAGCACGCAGTCAAACTGCACCTTAGTAAGAC 2424
       1068 AGCCACTGGCTGGCCAATGTGAAGTACCAGTTGAGGAGGACGACGGAACGAAATTCCTA 2127
                                                    831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1071 GCACAGCAAGTCACCCGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGAATAGC 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         832 ACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATG 891
                                                 772 AAAAACATGGACAAAGGCCACCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCAGA
                                                                                          2128 AAGAACCTGGACACAGGGCATCCTGTTTTCTTTTGCAACGATTGTGCCTCTCAGTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08828008
Patent No. 5939316
CENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Friemer, Nelson, B.
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 11
CCORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,008
FILING DATE: 27-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Pennie & Edmonds
F: 1155 Avenue of the Americas
New York
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TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION MUMBER: 37,071
REPERMCZDOCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.2%;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.5-
Local 79; Conservative
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Best Local Similarity 88.0
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 base pairs
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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; CLONE: 626570
US-09-023-655-773
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 TAAAAGAAAAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCCA 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CAAGAGGAAGGGCCGGCAGTCCAACTGGAACCCGCAGCA-CTTCTCATCCTGCAGGCCCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
WUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 314 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 GAAGCTGGAAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.8%; Score 113; DB 2; Length 282;
72.4%; Pred. No. 1.4e-25;
ve 0; Mismatches 60; Indels
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Fsh 22
                                                                                                                                               APPLICATION NUMBER: US/08/828,008
FILING DATE: 27-MAR-1997
PLASSIFICATION: 435
PLOSTICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 773, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
                                       MEDIUM TYPE: Diskette
COMPUTER: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTLEST, Laura A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 785:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-190-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.4%;
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Other
; LOCATION: 1...282
; OTHER INFORMATION: C;
; OTHER INFORMATION: US-08-828-008-3
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Sequence 15945, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

LENGTH: 31623
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFTCATION:
PRIOR ADDITOTOR
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; Pred. No. 0.66;
0; Mismatches
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Query Match
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## Sequence 1155626, Application US/09949016

## Sequence 1155626, Application US/09949016

## GENERAL INFORMATION:
## APPLICANT: VENTER, J. Craig et al.
## TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## PRIOR RPLIATION NUMBER: 60/231, 768

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-115533/c

Sequence 115533, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARAE: FastSEQ for Windows Version 4.0

SEQ ID NO 115533
                                                                                                                        1200 ACCATCCTGCTTCTGACATTGAACTCATTGAACTCCTCCTGACACCCCTGGCTCTGAGAAG 1259
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Pred. No. 0.28;
0; Mismatches 29; Indels
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Best Local Similarity 65.5%;
Matches 55; Conservative 0
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US-09-949-016-115626/c
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; ORGANISM: Human
US-09-949-016-115626
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SEQUENCE 115812, Application US/09949016
SEQUENCE 115812, Application US/09949016
SEQUENCE 115812, Application US/09949016
SERVERL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
STILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NOS: 207012
LENGTH: 6011
TYPE: DNA
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Sequence 115719, Application US/09949016

Sequence 115719, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOKINGT.
CURRENT APPLICATION NUMBER: US/99/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
SED ID NOS: 207012

SOUTHWARE: FREAKENCE PRESERVE OF WINDOWS Version 4.0
SEQ ID NO 115719
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2.9%; Score 37.6; DB 4; Length 601;
65.5%; Pred. No. 0.28;
cive 0; Mismatches 29; Indels
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Best Local Similarity 65.55
Matches 55; Conservative
                                                                  55; Conservative
                         Best_Local Similarity
Matches 55; Conserv
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ORGANISM: Human
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US-09-949-016-116091/c
                                                TYPE: DNA
ORGANISM: Human
US-09-949-016-115998
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ORGANISM: Human
; SEQ ID NO 115998
; LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 115905
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 00/29149,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-00-09
PRIOR PILING DATE: 2000-00-09
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
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                                                                         Score 37.6; DB 4; Length 601;
Pred. No. 0.28;
0; Mismatches 29; Indels
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                                                                            Query Match 2.9%;
Best Local Similarity 65.5%;
Matches 55; Conservative (
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Best Local Similarity
Matches 55; Conserv
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US-09-949-016-115998/c
; ORGANISM: Human
US-09-949-016-115812
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ORGANISM: Human
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GENERAL INCORMATION:
GENERAL INCORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOO1307
CURRENT PILING DATE: 2000-04-14
PRIOR PELLOCATION NUMBER: 60/241,755
PRIOR PELLOCATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR PELLOG DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTESEQ for Windows Version 4.0
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US-09-949-016-116184/c
is Sequence 116184, Application US/09949016
is Sequence 116184, Application US/09949016
is Sequence 116184, Application US/09949016
is Patent No. 6812339
is GENERAL INFORMATION:
is APPLICANT: VENTER, J. Craig et al.
is APPLICANT: VENTER, J. Craig et al.
is TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
is CURRENT APPLICATION NUMBER: US/09/949,016
is CURRENT FILING DATE: 2000-04-14
is PRIOR FILING DATE: 2000-10-20
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   Score 37.6; DB 4; Length 601;
Pred. No. 0.28;
0; Mismatches 29; Indels
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
2.9%;
      Query Match 2.9
Best Local Similarity 65.5
Matches 55; Conservative
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: P88ESEQ for Windows Version 4.0
; SEQ ID NO 116184
; LENGTH: 601
; TYPE: DMA
; ORGANISM: Human
US-09-949-016-116184
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214.2
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

 No.
 Score
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 1
 1288
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 1288
 8
 US-08-731-499-5
 Sequence 5, Appliance 100.0

 2
 1265
 98.2
 3322
 17
 US-09-764-864-528
 Sequence 373, Appliance 100.0

 4
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 59.8
 79.9
 US-09-764-864-193
 Sequence 193, Appliance 100.0

 5
 56.4
 51.0
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 US-09-764-864-193
 Sequence 193, Appliance 100.0

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 52.1
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 100-09-864-761-13203
 Sequence 13203, Appliance 100.0

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 Sequence 16736, Appliance 16736, Appliance 16736, Appliance 16736, Appliance 16736

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 US-09-864-761-16736
 Sequence 16736, Appliance 16723-860-25900
 Sequence 5900, Appliance 1670, Appli

Sequence 6999, Apsequence 1788, Apsequence 1795, App Sequence 273, App Sequence 165, App Sequence 165, App Sequence 5430, App Sequence 5430, App Sequence 5430, App Sequence 5430, App Sequence 19673, App Sequence 19673, App Sequence 19673, App Sequence 19673, App Sequence 773, App Sequence 6506, App Sequence 6780, App Sequence 174146, Sequence THEIR APPLICANT: COLLINS, Colin
APPLICANT: HWANG, Soo-In
APPLICANT: WGOPREY, Tony
APPLICANT: KOWBEL, David
APPLICANT: ROWNENS, Johanna
ITILE OP INVENTION: GENES FROM THE 20q13 AMPLICON AND
ITILE OP INVENTION: USES COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAEINIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,499
FILING DATE: 16-CT-1996 US-10-641-643-772 US-10-184-644-402 US-10-184-634-402 US-10-1029-386-6506 US-10-425-115-72371 US-10-719-99-6780 US-10-027-632-174146 US-10-156-761-5473 S US-10-156-761-10 US-10-146-731-10 US-10-146-731-10 US-10-062-674-1795
US-10-062-674-1795
US-10-863-119-165
US-09-764-864-137
US-09-764-864-137
US-10-040-862-5430
US-10-154-864-576
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US-10-10-198-995-19673
US-10-198-995-19673
US-10-198-8646-13601
US-10-198-8646-13601
US-10-198-8646-13601
US-10-198-8646-13601 NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco ALIGNMENTS CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/680,395
FILING DATE: 15-ULL-1996
ATTORNEY/AGENT INFORMATION: US-08-731-499-5
; Sequence 5, Application US/08731499
; Publication No. US20030148270A1
; GENERAL INFORMATION:
APPLICANT: GRAY, Joe W. GRAY, Joe W. COLLINS, Colin 20055 20 California : USA COUNTRY: CITY:

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CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGGACAAAATTTCTGAAAAACATG
                     TCAGTGGACCAGCAAAGCAAGGTGGAGCAAGAGATCTCCCGGGTATCGTCGGCTCAGAGG
                                                                                                                                                                                                                                                                                  901 TCAGTGGACCAGCAAGCTGGAGCAAGAGATCTCCCGGGTATCGTCGGCTCAGAGG
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                                                                                GACAAAGGCCACCCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCCTTCT
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Fublication No. US20030236392A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
TITLE OF INVENTION: No. US20030236392A1e1
TITLE OF INVENTION: NO. US20030236392A1e1
FULL OF INVENTION UNMBER:
CURRENT APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 3322
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CORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1288;
                                                                                                                                                                                                                                                                                                                          /note= "cDNA clone 41.1 with homology
to homeobox T shirt gene from
Drosophila"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1288; DB 8; Best Local Similarity 100.0%; Pred. No. 0; Matches 1288; Conservative 0; Mismatches 0;
                REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 23070-068910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                NAME/KEY: -
LOCATION: 1..1288
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                           TOPOLOGY:
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Db 3258 CCATCCTGCTTCTGACATTGAACTCCTCCTGACACCCTGGCTCTGAGAAGA 3317 Qy 1261 CTGCC 1265 Db 3318 CTGCC 3322	RESULT 3 US-09-764-864-628 US-09-764-864-628 Sequence 628, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223 CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17		ON: n equals a,t,g, or c) ON: n equals a,t,g, or c 60.0%. Score 773:	Similarity 100.0%; Pred. No. 4.38-231; 3; Conservative 0; Mismatches 0; Indels GTCTCCAGTGAAGTCTCAACTTTGCATAAAAGAAAAGGCCGGCAGTCCA	QY 574 CAGCATCTTCTGATTCTACAAGCCCAGTTTGCCTCGAGCCTCTTCCAGACATCAGAGGC 633	Db 215 AAATACTGCTGTCTGATCTGGGCCCACAAGAGCGTATGCAAATCTCTAAGTTTACGGGA 274 Qy	335 GGGGGACAAAATTTCTGAAAACATGGACAAAGGCCACCCATCTTTTATTGCAGTGAC 39 814 TGTGCCTCCCAGTTCAGAACCCCTTCTACCTCAGTCAATTCTAGAATCTCAGGGGGG 87 815 TGTGCCTCCCAGTTCAGAACCCCTTCTACATCAGTCACTTAGAATCTCACTGGGT 87 816 TGTGCCTCCCAGTTCAGAACCCCTTCTACATCAGTCACTTAGAATCTCACTGGGT 45 817 TGTGCCTCCCAGTTCAGAACCCCTTCTACATCAGTCACTTAGAATCTCACTGGGT 45	TTCCAAATGAAGGACATGACCGCTTGTCAGTGGACCAAGCAAAGCAAGGTGGAGGAAGGA	Db 575 GACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTGAGCAAACATGCGGTAAAA 634
121 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCTCC 21.78 TCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGGTCACCTTCCTGCTCC 181 AGCCCAAGTTCAAGCAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG 2238 AGCCCAAGTTCAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAATGTCATGGACAAG	QY 241 CCGGTCTTGAGTCCTCCACAAGGTCAGCCGGGTGTCCAGGCGCTACTTTTGAG 300 Db 2298 CCGGTCTTGAGTCCTGCCTCCACAGGTCAGCGTGTCCAGGCGTTTTGAG 2357 QY 301 AACAGCGATCAGCCCTTGACCTGACCAAGGTCCAAGGCGCTTTTGAG 2357 Db 2358 AACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAGCAAGAAGACCGAGTCCTCGCAA 360 C 361 GCACAATCAGCCCATTGACCTGACCAAGTCCAAAAGCCAAGACCGAGTCCTCGCAA 2417 QY 361 GCACAATCTTGATGTCCCCACCTCAGAAAGCCCAAGAAAGCCGACATGGTC 420	421 AAAGTCGTCCCCAAAGCCACCCCCAAAGCCACCTCTTCTCTCCCCGGGTCCCCCCATG 421 AAAGTCCTCCCCCAAAGCCACCCCCAAAGCCAACGCTCCTCCTCCTCCTCGGGTCCCCCCCTG 481 AAGTCGCCCCCAAAGCCACCCCCAAAGCCATGCTTTTGAGATTCTCCCTCC		661 CAGAGCGTATGCAATTCTTAAGTTTACGGGACTCTCAATGACCACTATCAGTCACTGG 2718 CAGAGCGTATGCAATTCTTAAGTTTACGGGACTCTCAATGACCACTATCAGTCACTGG 2718 CAGAGCGTATGCAATTCTTAGAGAAACGGGCGGGAAATTTTTGAAAAACATG	Db 2778 CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGACAAAATTTCTGTTTTTTTT	OY 841 ACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCGGTTG 900 Db 2898 ACCTACATCAGTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCGGTTG 2957 Qy 901 TCAGTGGACCAAAGCAAGGAGACAAGAGATCTCCCGGGTATCGTCGGCTCAGAGG 960 Dh 2958 TCAGTGCACCAAAAGCAAGAAGTTCTCCCGGGTATCGTCGGCTCAGAGG 317	1021 TGTCGGAAACAATGCGGCGAAGACACAGACTCGCGGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGAGGTTTCGTTTGTTGGTTTCGAGGAACAATGCGCGAAGGAGCACACAGAGCGACACAGAGCACACAGAGCGACACAGGAGCACACAGGAGCACACAGGAGCACACAGGAGG	3078 TGTCGGACATTGTGAGCAACATGCGGTAAAACTCCACCTAAGCAAACGCACAGGAAG 3137	OY 1201 CCATCCTGCTTCTGACATTGAACTCCTCCTCGACACCCCTGGCTCTGAGAAGA 1260

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MERICAMI: Penni, Sharron G.

APPLICANY: Rank, David R.

ITILE OF INVERTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

ITILE OF INVERTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPRENCE: Accord.ca.x.l.

CURRENT FILING DATE: 2000-05-33

PRIOR FILING DATE: 2000-05-34

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR PRIOR DATE: 2001-01-30

PRIOR PRIOR PRIES DATE: 2001-01-30

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994 GACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTGAGCAAACATGCGGTAAAA 1053
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                         492 GACTCTAAATTCAAGTGTAAGTTGTGGTGTGTGGGACATTTGTGAGCAAACATGCGGTAAAA
                                                                                                                       GTGGATGAAGAATAGCTCTGCAGGACGAATGCCTTAGTTTCCACTTTCCAGCCTGGATCC
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Patent No. US20020048763A1
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                                                       CTCCACCTAAGCAAAACGCACAGCAAGTCACCCGAACACCATTCACAGTTTGTAACAGGC
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                         CTCCACCTAAGCAAAACGCACAGCAAGTCACCCGAACACCATTCACAGTTTGTAACAGAC
                                                                                                                       GTGGATGAAGAATAGCTCTGCAGGACGAATGCCTTAGTTTCCACTTTCCAGCCTGGATCC
                                                                                                                                                   GTGGATGAAGAATAGCTCTGCAGGACGAATGCCTTAGTTTCCACTTTCCAGCCTGGATCC
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Patent No. US20020132753A1

GENERAL INPORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ3

CURRENT APPLICATION NUBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 193

LENGTH: 799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-764-864-193
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Best Local
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1504 TGCGCCCTCGCCAACCACGCCCCGGCCCTGCCATGCATCAACCCACTCAGCGCCCTGCAG 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1444 GAGGGCAGCGAGAGAAGGAGAAACCCCAGCCCCTGGAGCCCCACATCTGCTCTGAGCAATGGG
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               CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 200
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llarity 100.0%; Pred. No. 4e-152;
Conservative 0; Mismatches 0
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL
US-09-864-761-16736
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ORGANISM: Homo sapiens
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521; Conserv
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Matches 52
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Patent No. US20020048763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENER EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                                                                                                                                    51.0%; Score 656.4; DB 9; Length 2012; 99.8%; Pred. No. 1.4e-194; ive 0; Mismatches 1; Indels 0;
                                            TYPE: DNA ORGANISM: Homo sapiens (CHANISM: Homo sapiens) FRATURE: FRATURE: FRATURE: CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1 (CTHER INFORMATION: BY HIT: AF207880.1, EVALUE 0.00e+00 (CTHER INFORMATION: BYT HUMAN HIT: H12950.1, EVALUE 0.00e+00 (CTHER INFORMATION: SWIËSEROT HIT: P22265, EVALUE 1.00e-07 US-09-864-761-33203
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Matches 657; Conservative
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SEQ ID NO 33203
LENGTH: 2012
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                                                                                                                          1702 CCGGTCCACAAGAGGAAGGGCCGGCAGTCCAACTGGAACCCGCAGCACCTTCTCATCCTG 1761
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Publication No. US20030224461A1

GENERAL INFORMATION:

JAPPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antiboc CURRENT APPLICATION NUMBER: US/10/091,414

CURRENT APPLICATION NUMBER: 2020-03-07

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 392

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 288

LENGTH: 3604
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COTHER INFORMATION: n equals a,t,g, or US-10-091-414-288
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Pred. No. 4.6e-111;
0; Mismatches 381; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5420, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROBER et al.
TITLE OF INVENTION:
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILION NUMBER: US/09/764,891
CURRENT FILION DATE: 2001-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9420
LENGTH: 3604
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; OTHER INFORMATION: n equals a,t,g, or
US-09-764-891-9420
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NAME/KEY: SITE
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                                                                                                                                                                    APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Gordon G.
APPLICANT: Fechtel, Kinlary
APPLICANT: Fechtel, Kinlary
APPLICANT: Fechtel, Kinlary
APPLICANT: Respired, Michael J.
APPLICANT: Respired, Michael J.
APPLICANT: Respired, Richard J.
APPLICANT: Graham, James R.
APPLICANT: Graham, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2587 cricializado de contra de contra contra de contra con
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62.4%; Pred. No. 4.8e-111;
tive 0; Mismatches 381;
Application US/09823245A . US20020039760A1
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NAME/KEY: misc_feature
LOCATION: 3870
OTHER INFORMATION: n = a,t,g, or
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Sequence 409, Applica
Publication No. US200
GENERAL INFORMATION:
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Sequence 5900, Application US/10723860

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Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginaburg, Wendy M.
APPLICANT: Ginaburg, Wendy M.
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05812.0193 NPUS01

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR PLILNG DATE: 2003-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn version 3.2

LENGTH: 5065
                             2679 CAGTCAAACTGGAACCCCCAGCACCTCCTGATCCTCCAGGCCCAGTTTGCCGCCCAGGCTC 2738
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NAME/KEY: misc feature
LOCATION: (4376)..(4392)
COTHER INFORMATION: n is a,
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ORGANISM: Homo sapiens
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US-10-723-860-2953

US-10-723-860-2953

Sequence 2953, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: Alazia, Natasha
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
APPLICANT: Journal Compositions & TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PLING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin Version 3.2

SEQ ID NO 2953
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                                                        3004 TIGGCCCCCCAGAAGAGGTGCACATCTCGAAGTTTACTGGGCTCTCCATGACCACCATC 3063
                                                                                                                                              3184 ACTGCTTCTACATACATAAGTCATTTGGAGACACACACTTGGGCTTCAGCCTGAAGGATCTC 3243
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                                                                                                                                                                                                                                                                                                                                                                                                       892 ACCCGCTTGTCAGTGGACCAGCAAGCAAGGTGGAGCAAGAGATCTCCCGGGTATCGTCG 951
                        CTGGGCCCACAGAGCGTATGCAAATCTCTAAGTTTACGGGACTCTCAATGACCACTATC 711
                                                                                                                                                                                                                                                                                                            ACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATG 891
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                                                                                                                   GTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCAACTTTGCATAAAAGAAAAGGCCGG
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; ORGANISM: Homo sapiens
US-10-723-860-2953
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; SEQ ID NO 6999
; LENGTH: 5065
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (520)...(614)
; OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                       | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (4376)..(4392)
| OTHER INFORMATION: n is US-10-723-860-6999
                                                                                                                                                                                                                                                                                                                                                        Similarity
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US-10-723-860-7288
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Matches 469
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Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natusha
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                                                                                                                      8644 TCGCCGCTACGCGAGAATGCCTTGTCAGATATATCCGATATGCTGAAGAACTTGACAGAG
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                                                                          TCCCCACCTCAGAAGCACGCTCTGTCTGACATCGCCGACATGGTCAAAGTCCTCCCCAAA
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                               15;
                            Indels
    Best Local Similarity 62.2%; Pred. No. 7.1e-74;
Matches 469; Conservative 0; Mismatches 270;
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SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                             Length 5065;
                                                                                                                                                                                                                                                  0; Mismatches 270; Indels
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Pred. No. 7.1e-74;
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976 GCTGCCGAAGAGGACACACAGACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTG 1035
                                                            329 TCCCCCGAGGAAGACCTGGGGACTTCCTATCAGTGCAAACTTTGCAATCGGACCTTTGCC 3288
                                                                                                                 AGCAAACATGCGGTAAAACTCCACCTAAGCAAAACGCACAGCAAGTCACCCGGAACACCAT 1095
                                                                                                                                               3289 AGCAAGCACGCTGTTAAACTTCACCTTAGCAAAAACACACGGGAAATCTCCGGAAGACCAC 3348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friemer, Nelson, B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC
DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 GAAGCTGGAAATGGATGTCAGGCGCTTTGAGGATGTCTCCAGTGAAGTCTCGAACTTTGCA
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NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-071
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFAX: 212-869-8864
TELEXX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,707
FILING DATE: 23-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/828,008
FILING DATE: 1997-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
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LOCATION: 1...282
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1144 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09739707
Patent No. US20020142298A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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Matches 437; Conservative
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US-09-739-707-1
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Sequence 7288, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Glosburg, Wendy M.

APPLICANT: Glosburg, Wendy M.

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7228
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Pred. No. 7.1e-74;
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LOCATION: (4376)..(4392)
OTHER INFORMATION: n is a, c,
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62.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 469; Conservative
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                                             GCCCTGCAGTCCGTCCTGAACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCT 171
                                                                                                                                                                                                                                                                              TGTCACCGGTCCACAAGAGGAAGGCCGGCAGTTGCCAACTGGAACCCGTCAGCACCTTC
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                                                                   232 ATGGACAAGCCGGTCTTGAGTCCTGCCTCCAC---AAGGTCAGCCAGCGTGTCCAGGCGC
                                                                                                                                                                                                                                         2570 CTGGGACAAGCACAGTGTACCCCCCCCCCCTGTGAAGCAGGCCGATGCCATCGACCGC
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TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFERENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: US 09/625,102
PRIOR APPLICATION NUMBER: US 09/625,102
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL PROGram
SEQ ID NO 1795
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16.6%; Score 214.2; DB 17; Length 4839;
Best Local Similarity 59.3%; Pred. No. 9.2e-56;
Matches 629; Conservative 0; Mismatches 393; Indels 39;
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CTHER INFORMATION: a, t, c, g, or other US-10-062-674-1795
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OTHER INFORMATION: Incyte ID
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/gene="DKFZp686F07129
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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SOURCE	HILC.	
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REFERENCE		
AUTHORS	, Krieger, S., Regiert, T., Rittmueller, C., Schwag	
	Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and	
	Wiemann, S.	
CONSRIM	The German cDNA Consortium	
TITLE	Direct Submission	
JOURNAL		
	Neuherberg, GERMANY	
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer	
	KESSEZICH CHILCEI (U.D.K.E.); Bildall S.W.Hermaningurtz-Heituelluellue; Commission http://www.mail.com/localists/pic/localists/p	
	sequenced by Embb (Eulopean Molecular Blology Labolacoiles) Heidelberg/Germany) within the CDNA semiencing consortium of the	
	octimen Genome Froject; This clone (DKF2n686F07;29) is available at the RZPD Deutsches	
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	rurruer information about the clone and the sequencing project is	
	available at http://mips.gsf.de/projects/cdna/.	
FEATURES	Location/Qualifiers	
source		
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	/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host	
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	/dev_stage="adult"	
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)	/gene="DKFZp686F07129"	

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AK045693 1705 bp mRNA linear HTC 03-APR-200 Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230304M06 product:TEASHIRT 2 (FRAGMENT) homolog [Mus musculus], full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                         CTGGCCAACGTCAAGTACCAGCTTAGGAAAACGGGCGGGACAAAATTTCTGAAAAACATG
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Carninci, P. and Hayashizaki, Y.
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| proteIn_id="BA23459.1"
| db_xref="GI:.6837547"
| translation="MKSLKQCGKESPHEEATSFSQPEGESFSKIEPPSESRKAEPCPL
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                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation 6 f 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                               FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product; TEASHIRT 2 (FRAGMENT) homolog [Mus musculus] (SPTR|Q9JL71, evidence: FASTY, 98.6%iD, 6.2%length, match=207)
                                                                                                                                                                                                                  Team and
                                                                                                                                                                                                                                FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II
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|clone_lib="RIKEN full-length enriched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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DVSSEVSTLHKRKGRQSNWNPQHLLILQAQPASSLFQTSGGKYLLSDLGPQERMQISK
FTGLSMTTISHWLANVKYQULRKTGGTKFLKNMDKGHPIFYCSDCASQPRTPGTYISHL
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                                                                                                                                                                                          AGAAGGAGAAACCCCCAGCCCCTGGAGCCCCACATCTGCTCTGAGCAATGGGTGCGCCCTCG
                                                                                                                                                                                                         CAAGCACAATTTCCATGTTCCACAAGTCGAATCTCAAATGTCATGGACAAGCCGGTCTTGA
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                                                                                                                                                           Gaps
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                                                                                                                           Length 1705;
                                                                                                                                                                                                                                                                                                                     ACAATCACTTGGGCAAAGCCACGGAGCCCTTGCGCTCACCTTCCTGCT
                                                                                                                                                           Indele
                                                                                                                          Score 793.6; DB 3;
Pred. No. 2.4e-206;
0; Mismatches 124;
                                                                                                                           Query Match 61.6%;
Best Local Similarity 87.4%;
Matches 881; Conservative
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                    487 ACAAAGGCCACCCCATCTTTTATTGCAGTGACTGTGCCTCNCAGTTCAGAACCCCTTCTA
                                                                                                                                                                                                                                                                                                                                        307 CTCCAGAAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAAGTTGTGCT
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                                                                                                                                                                                                                                                                 367 CAGTGGACCAGCAAAGCAAGGTGGAGCAAGAGATCTCCCGGGTATCGTCGGCTCAGAGGT
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                                                                                                                        CCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCGCTTGT
                                                                                                                                                                    427 CCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCGCTTGT
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/db_xref="taxon:9606"
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Nww-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1472 Std Error: 0.00
Seq primer: -40UP from Giber
High quality sequence stop: 412.
Location/Qualifiers
                                                                                                                                                                                                                                      AI889627 17-MAR-2000 wmS9903.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2440276 3' similar to TR:060534 060534 ANTIGEN NY-CO-33. ;, mRNA sequence.
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/clone_lib="NUICGAP_Ut2"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 8.7e-176;
0; Mismatches 15; Indels
                                                                       AAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAAGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 97.7%;
Matches 710; Conservative
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Unpublished (1997)
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AI889627/c
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/clone="IndexDillows"
/clone="IndexDillows"
/clone="IndexDillows"
/tissue_type="whole brain"
/dev stage="mbryol5.5 dpc"
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/clone lib="NIH BMAP EXO"
/clone lib="NIH BMAP EXO"
/clone lib="IndexDillows to the liberary was constructed according to Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EorN I adaptor, digested with Not I, and then cloned directionally into pXx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), 'Hemin Chin, Ph.D., program coordinator:"
                                                                      CB249889 178 bp mRNA linear EST 15-JUL-2003 UI-M-EX0-byo-k-23-0-UI.rl NIH BMAP_EX0 Mus musculus cDNA clone IMAGE:5720974 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capbs r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 778;
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88.9%; Pred. No. 1.1e-160;
iive 0; Mismatches 84;
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/strain="C57BL/6"
                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                              CB249889.1 GI:28389782
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/lab host="DH10B (Life Technologies)"
/clone lib="NCI CGAP BII"
/none lib="NCI CGAP BII"
/note="Torgan Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP EII is a normalized CDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonuclectide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(GT) B tail. The sequence tag for this library is
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Pred. No. 1.6e-174;
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TAG_SEQ=ACACTTGCAC"
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                                      /clone="IMAGE:2791015"
/tissue_type="moderately-differentiated endometrial
denocarcinoma, 3 pooled tumors"
/lab host="DHID5"
/clone_lib="NCI_CGAP_Ut2"
/note="Organ: uterus; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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Sus scrofa (pig)
Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AGTGACTGTGCCTCNCAGTTCAGAACCCCTTCTACCTACATCAGTCACTTAGAATCTCAC
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                                                                                                                                                                                                                                                                                  1 47.6%; Score 613.6; DB 2; Similarity 97.3%; Pred. No. 5.2e-157; 2; Conservative 0; Mismatches 17;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Gequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.lln! gov/image/html/iresources.shtml
Seg primer: -40UP from Glbco
High quality sequence stop: 425.
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(Dases 1 to 639)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Gancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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                        TCAGACGCTTCGAGGATGTTTCGAGCGAAGTCTCCACTTTGCACAAAAGGAAAGGCCGGC
                                                                                                                                                                                                                                                           TCCAGACATCAGAGGGCAAATACCTGCTGTCTGATCTGGGCCCCACAAGAGCGTATGCAAA
                                                                                                                                                                                                                                                                                         TCCAGACCTCAGAGGGCAAATACCTGCTTTCTGACCTGGGCCCCCAAGAGCGGGTGCAAA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCGAAGAGACACAGACTCTAAATTCAAGTGTAAGT 1015
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Homo sapiens
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RESULT 6 AW516191/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

source

FEATURES

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/clone="INGESTINGS"
/clone="INGESTINGS"
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/dev stage="newborn(1,5,15,15,498)"
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/ince="Corgan: Bye; Vector: pYX-Asc; Site 1: EcoR I;
/clone_lib="NHI BMAP_HU0"
/clone_lib="NHI BMAP NOT Size fraction a 1% agarose
gel.:First strand cDNA was size fractionated on a 1% agarose
gel.:First strand cDNA was size fraction, ligated
yrimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. "Chases 1 to 671)

Si "Chases 1 to 671)

In "Chases 1 to 671)

In H-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This.clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                       671 bp mRNA linear EST 29-APR-2004
UI-M-HUO-cgs-i-15-0-UI.rl NIH_BMAP_HUO Mus musculus cDNA clone
UNAGE:30667886 5', mRNA sequence.
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91.4%; Pred. No. 1.3e-132;
ive 0; Mismatches 52;
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                              1121 AAGAATAGCTCTGCAGG 1137
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                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
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1 (bases 1 to 892)
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine BST collection using a normalized library constructed from embryos representing early developmental stages
Unpublished (2003)
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indels
                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%; Score 525.8; DB 7; 90.8%; Pred. No. 7.3e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     cross match v0.990329.
Plate: TWW8025 row: A column: 10
Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .892
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/clone liberCSEQCHN03"
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Site li EcoRI; Site 2: Not1; This normalized library was constructed from I million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
Following this first strand synthesis reaction. Following this first strand spatients digested with was blunted, ligated to NotI adapters, digested with EcoRI; size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAAAGAAAAGGCCGGCAGTCCAACTGGAATCCTCAGCATCTTCTGATTCTACAAGCCC
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                                                                                                                                                                                                                                                                                                                                                                 39.8%; Score 512.8; DB 5;
83.9%; Pred. No. 2.6e-129;
live 0; Mismatches 112;
  'lab host="DH10B"
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Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus (chicken)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (base 1 to 770)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUZ04906 1770 bp mRNA linear EST 25-NOV-2002 604157793F1 CSEQCHN03 Gallus gallus cDNA clone ChEST1008j24 5',
                                                                                                                                                                                                                                                                                                                                                                                          950 CGGCTCAGAGGTCTCCAGAAACAATAGCTGCCGAAGAGGACACAGACTCTAAATTCAAGT 1009
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                                                                                                                                                                                                                                                                                                                                 361 TGACCCGGATGGCGGCTGACCAGCAAAGCAAGGTGGAGCAGGAGATCTCCCGGAGTGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TCAGCCACTGGCTAGCGTCAAATACCAGCTTAGGAAAACAGGTGGGACAAAGTTCC
                                                                                                                                             TGAAAAACATGGACAAAGGCCACCCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCA
                                                                                                                                                                                                                              GAACCCCTTCTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACA
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University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
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1.770
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST1008]24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole embryo"
/dev_stage="20-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:25369490
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240

718 300 778 360 838 420 1018

597

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480

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CR745711 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGp971N1484 ;
IMAGE:2010852 5', mRNA sequence.
                                                                                                                                                                                                                                                                  GAGGICTCCAGAAACAATAGCIGCCGAAGAGAACA-CAGACTCT-AAATTCAAGTGTAAG 1014
                                                                                                                                                                                                                                                                                                                                                           1015 TIGIGCIGICGGACA-TITGIGAGCAAACAIGCGGIAAAACICCCACCIAAGCAAAACGCA 1073
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836
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                                                                                                                                                                                                          480 GATGGCGGCTGA-CAGCAAAGCAAGGTGGAGCAGGAGATCTCCCGAGTGTCGTCGGCTCA
                                                                                                                                                                                                                                                                                              539 GAGGICTCCAGAAACAATAGCTGGCGAAGAGGACACCAGACTCTAAAATTCAAGTGTAAG
                                                                                                                                                                                                                                                                                                                                                                                    599 TTATGCCGTCGGACATTTTGTGAGCAAACACGCAGTAAAACTTCACCTAAGCAAAAAACGC
                                                                                                               CATGGACAAAGGCCACCCATCTTTTATTGCAGTGACTGTGCCTCCCAGTTCAGAACCCC
                    837 TICTACCTACATCAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCG
                                                                                                                                                                              897 CTTGTCAGTGGACCAGCAAAGCAAGGGGGGGGAAGAGAGTCTCCCGGGGTATCGTCGGCTCA
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1 (Dases 1 to 494)
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., E., Peters, M., Radelof, U. and Schneider, D.
I.M.A.G.E. CDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1074 CAGCAAGTCACCGGAACACCATTCACAGTTTGTAACAGACGTGGATGAAGA 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Inge Ariar
Contact: Inge Ariar
Contact: Inge Ariar
Contact: Inge Ariar
RZPD Deutsches Ressourcenzentrum fuer Genomforschung Gmbi
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzbd.de
RZPD; IMAG5971N484.
RZPD; IMAG5971N484.
RZPD Deutsches Ressourcenzentrum fuer Genomforschung Gmbi
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 110
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/db_xref="taxon:9606"
/clone="IMAGp971N1484 ; IMAGE:2010852"
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Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Gilbert Smith, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhl.gov

Plate: LLAM9261 row: 1 column: 12

High quality sequence stop: 676.

Location/Qualifiers

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/ db xref="taxn.i."
/ db xref="taxn.i."
/ clone="lMAGE:4015643"
/ tasue_type="tumor, metastatic to mammary"
/ lab_host="bH108"
/ clone lib="NCI_CGAP_Lu30"
/ note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
                                                                   BF140337 953 bp mRNA linear EST 24-OCT-2000 601787846F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015643 5',
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                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I tbasea I to 9310; NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                         BF140337.1 GI:10979377
                                                                                                               mRNA sequence.
                                                                                                                                                                                                                               Mus musculus
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/Loue=Indusity 1922/
/Lab host="DRIOB" | /Clone lib="NCI CGAP Kid3" | /Clo
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 471.
Location/Qualifiers
                                                                                                              organism="Homo sapiens'
                                                                                                                                                                                                   /clone="IMAGE:1473227"
                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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www-bio.llnl.gov/bbrp/image/image.html
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the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                     1 AGAACAGCGATCAGCCCATTGACCTGACCAAGTCCAAAAAGCAAGAAAGCCGAGTCCTCGC
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                                                                                                                                      Length 494;
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Pred. No. 6.5e-124;
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                                                                                                                                      Query Match
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Matches 493; Conservative
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Pahrenkrug,S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AGTITICCACITICCAGCCIGGAICCCCICACACACAGACCCITCTICGITGCACCATCCIG
                                                                                                                            849 CAGTCACTTAGAATCTCACCTGGGTTTCCAAATGAAGGACATGACCCGCTTGTCAGTGGA
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36.9%; Score 475.4; DB 1; Length 477; 99.8%; Pred. No. 4.4e-119; ive 0; Mismatches 1; Indels 0
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AGENCOURT 8474842 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6310221 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                 Mus musculus
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13732 row: column: 22

High quality sequence start: 79

High quality sequence stop: 516.
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                                                                                                                                                                                                                                                                                                                                                                             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
        984 AGAGGACACAGACTCTAAATTCAAGTGTAAGTTG 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.0%; Score 438; DB 5;
88.0%; Pred. No. 1e-108;
iive 0; Mismatches 65,
                            146 AGAGGACACGGACTCTAAATTCAAGTGACAAATG
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                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.9903129.
Plate: 76 row: K column: 24
Seq primer: GTAATACGACTCACTATAGGG.
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Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib= MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue From testis, thymus, semitendomosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 CTCCGAGGGAAATACCTGCTGTCCGACCTGGGCCCGCAAGAGGGGATGCAGATCTCGAA
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                                                                                                                                                                      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.1
Best Local Similarity 88.2
Matches 506; Conservative
                                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
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Fax: 402 762 4396
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                      EST 20-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="monus"
/th _xref="taxon:9913"
/th _xref="taxon:9913"
/th _xref="taxon:9913"
/lab_host="monus"
/lab_host="MARC 3BOV"
/note="Vector: pcWV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 581)
Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wary, J.D.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
750
                                                                    451 GGACTCTCCCATGACCACAGCACTGGCTGGCTAACGTCAAATACCAGCTTAGGAAA 510
                                                                                                                   ACGGGCGGGACAAAATTTCTGAAAAACATGGACAAAGGCCACCCCATCTTTATTGCAGT 810
                                                                                                                                    GACTGIGCCTCCCAGTTCAGAA-CCCCTTCTACCTACATCAGTCACTTAGAATCTCACCT 869
                                                                                                                                                                                                      571 GACTGTGCGTCCCAGTTCACAACCCCCCTTAACTTCAGCCCCCTAAAGTCTCCCCT 630
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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967078 MARC 3BOV Bos taurus CDNA 3', mRNA sequence.
CK775937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                       GGGGCTTCCCAATGAAAGGACATGACCC 658
                                                                                                                                                                                                                                                  870 GGG--TITCCAAATGAAGGACATGACCC 895
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Seq primer: GTAATACGACTAAAGG.
Location/Qualifiers
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GCTGCCGAAGAGGACACAGACTCTAAATTCAAGTGTAAGTTGTGCTGTCGGACATTTGTG 1035
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AC117569 Homo sapi
AC11077 Homo sapi
AC11077 Homo sapi
AC134558 Plasmodiu
AC055393 Sequence
AC655393 Sequence
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AC02491 Homo sapi
AC13625 Homo sapi
AC137785 Homo sapi
AC0079811 Homo sapi
AC007981 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
1 (bases 1 to 455)
Gray,J., Collins,C., Hwang,S.-i., Godfrey,T., Kowbel,D. and
AC129169 I
CQ003853 3
AC014823 AC004948 AC004948 AC11824 AC11824 AC11821 AC108123 AL021939 I
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100.0%; Pred. No. 6.2e-102;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes from the 20013 amplicon and their uses
Patent: US 5892010-A 8 06-APR-1999;
Location/Qualifiers
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Sequence 8 from patent US 5892010.
AR070331.1 GI:7221219
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             CQ003853
AE014823
AC004948
HS1100E15
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AC108123
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AC137788
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AC137785
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Best Local Similarity 100.
Matches 455; Conservative
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BD085732 Genes fro
BC071570 Homo sapi
AB002385 Human mRN
AC006321 Homo sapi
AR469583 Sequence
AR404162 Sequence
AR404162 Sequence
AC0372 Homo sapi
BC034040 Homo sapi
G19707 human STS A
AC117965 Rattus no
AC11766 Rattus no
AC11766 Mus muscu
AC118023 Mus muscu
AC118023 Homo sapi
AC084013 Homo sapi
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                                                                                                                                                                                      1 GAAATCAGAAGTTTAATATG.......ATTGTCCTATTTCNGGGGGT 455
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                                                                                                                                                                                                                                                                                        9416466
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                            4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - nucleic search, using sw model
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BD085732
BC071570
AB002385
AC066321
AR365583
AR404162
HSU81561
AC034040
HSU66702
G19707
AC117965
AC117966
AC110335
AC110335
AC118633
                                                                                                                                                                                                                 IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                                                                          US-08-731-499-8
                                                                                                                                                                                                                                                                                                                                                                                                                                gb_ba: *
gb_htg: *
gb_om: *
gb_ow: *
gb_ox: *
gb_pr: *
gb_pr: *
gb_ro: *
gb_ets: *
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428
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                                                                                                                                                          Title:
Perfect score:
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240

CTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCAT

241 CATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCTA 300

121 TICATITICGATIAATIAAATICCAGATAGAGAGAAGIAATITITCGGAAAAGAAATGATAG 180

TTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATAG

121

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181

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211959 105604 106216

91.1 123.1 18.9 16.9 16.4 10.9

105 86.2 85.6 76.8 74.6 74.6 50.4

6 8 9 10

Result Š.

	BC071570 Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2, mkNA (cDNA clone MGC:87154 IMAGE:4375815), complete cds. BC071570.1 GI:47939488 MGC. Homo sapiens (human) Homo sapiens (human) Homo sapiens (cariniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases It o. 4723) Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschll, S. F., Zeeberg, B., Buteleow, T., Max, S. I., Wang, J., Habb, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Folatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,		Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NHH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Email: cgapbs-r@mail.nih.gov CONA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki CONA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) CONA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
ò a ò a ò a ò a ·	RESULT 3 BC011570/C LOCUS DEFINITION ACCESSION VERYORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE	REMARK COMMENT
Db 241 CATTCTGTCCGCTCAGTAGGCCGTGTTCCTCTGGTAGGGCCTTTGGAGAGTCATCTA 300 Oy 301 TCTAAGATGGAGAATGCTGTGGGAAGGCGGATGGAGGTGCTTTTCTACGCTGAACC 360 Db 301 TCTAAGATGGAGAATGCTGTGGAAGGCGGGATGGATTTTCTACGCTGAACC 360 Oy 361 CCACAGGAAATGCTGTGGAAGGCGGGGATGGGTTTTTTTT	DEFINITION Genes from the 20q13 amplicon and their uses. ACCESSION BD085732 BD08573	PI JOAN-1979 US DW/085532 PI JOHN-1979 US WW/085532 PI JOHNAMA ROWBEL, PI JOHNAMA ROWBEL, PU JOHNAMA ROWBEL, PU JOHNAMA ROWBEL, CC DESCRIPTION OF Artificial Sequence:20sa7 COCATION OF TWO OF T	

PRI 10-MAY-2002

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Nagase,T., Ishikawa,K., Nakajima,D., Ohira,M., Seki,N.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
VII. The complete sequences of 100 new cDNA clones from brain which
can code for large proteins in vitro
DNA Res. 4 (2), 141-150 (1997)
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keegslpagagealsdglqlevqpseeeargyivtdrdpeplrpeegrrlvedvarllgv
pssafadvevlgpavtfkvsanvqnvttedvekatvdnkdkleetsglkilqtgvgsk
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WSEEPVQSNMDISTGHMILSYMEDHLKONKONRLEKEWEALCAYQAEPNSSFVAQREENV
PKONRSLAVLTYDHSRVLLKAENSHSHSDYINASPIMDHDPRNPAYIATQGPLPATVAD
                                          4346 CCCACACAGGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCCTTCCATGTGATCATC 4287
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RSFYLKNLQTNETRTVTQFHPLSWYDRGVPSSSRSLLDFRRKVNKCYRGRSCPIIVHC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
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/clone_lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of th
/note="This sequence was obtained by subcloning of th
/ragments derived from two cDNA clones (1 - 506 was
derived from fj12719 and 507 - 4944 was derived from
hj00020)."
                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                              AB002385 4944 bp mRNA
Human mRNA for KIAA0387 gene, partial cds.
AB002385
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                                                                                                                                                    453
                                                                                                                                                        CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG
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/gene="KIAA0387"
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KIAA0387.
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VERSION
KEYWORDS
SOURCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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MEDLINE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                                                                       셤
                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 167 Row: b Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19743910. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PESSISSEETTAGENEESTINGSON INDUSTRICTURESSEETTAGENEETTAGENEESTESEETTAGENEETTAGE
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REGGAALANALRRHLPFLEALSQAPASDVLARTHTAQDRPPAEGDDRFSESILTYVAH
TSALTYPPGPRTQLREDLLPRTLGQLQPDELSPKVDSGVDRHHIMAALSAYAAQRPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGEGSLEPQYLLRAPSRMPRPLLAPAAPQKWPSPLGDSEDPSSTGDGARIHTLKUDL
QRQPAEVRGLSGLELDGMAELMAGLMQGVDHGVARGSPGRAALGESGEQADGPKATLR
GDSFPDDGVQDDDDRLYQEVHRLSATLGGLLQDHGSRLLPGALTFARPLDMERKKSEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4705 GAAATCAGAAGTTTAATATGACACAATTAAATATATATTTGTATATCTCACACGGAGGTTT 4646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4585 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 4527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9526 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 4467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCTAAGATGGAGGAATGCTGTGGGAAGGGGGGGATGGAGGTGCGTTTTCTACGCTGAAC 4347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="synonyms: IA-2beta, IAR, ICAAR, KIAA0387, PTPRP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Brain, hippocampus"
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'product="PTPRN2 protein"
                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAH71570.1"
db_xref="G1:47939489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="LocusID:5799"
/db_xref="MIM:601698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |db xref="LocusID:5799"
|db_xref="MIM:601698"
|1200. .2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="PTPRN2"
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420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP5-991P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:SP6
vector_side:right"
92955. .118947
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Best Local Similarity 99.1%;
Matches 450; Conservative
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Homo sapiens chromosome UNK clone RP5-991P5, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
SDGAGRSGTYVLIDMVLNKMAKGAKEIDIAATLEHLRDQRPGMVQTKEQFEFALTAVA
EEVNAILKALPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4403 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGCCTTTGGAGAGTACCATCT 4644
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                                                                                                                                                                                                                                                                    1882 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 4823
                                                                                                                                                                                                                                                                                                                                                1822 ATTCATTTCGATTAATTTCCAGATAGAGAAGTAATTTT-GGAAAAGAATGATA 4764
                                                                                                                                                                                                                                                                                                                                                                                                              4763 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 4704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Aug 24, 2000 this sequence version replaced gi:8018216.
                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                  CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                                                                                                                                                          ATTCATTTCGATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC 419
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 118947)
                                                                                                                                                                                                                                                                                                                                                                                        180 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA
                                                                                                                                                       GAAATCAGAAGTTTAATATGACACAATTAAAATATATTTGTATATCTCACACGGA-GNTT
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Center code: WIGSC
                                                                           Length 4944;
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                                                                         Score 428; DB 9;
Pred. No. 1.2e-95;
0; Mismatches 2;
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AC006321.3 GI:9887769
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Waterston, R.H.
                                                                           Query Match
Best Local Similarity 99.1%;
Matches 450; Conservative
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KEYWORDS
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29987 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 30045
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                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: plasmid; 15%
Chemistry: Dye-primer ET; 85% of reads
Chemistry: Dye-terminator Big Dye; 15% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 117806 bases at least Q40
Consensus quality: 118306 bases at least Q30
Consensus quality: 118463 bases at least Q20
Insert size: 132000; agarose-fp
Insert size: 11847; sun-of-contigs
Quality coverage: in Q20 bases; garose-fp
Quality coverage: in Q20 bases; sum-of-contigs
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Pred. No. 1.4e-95;
0; Mismatches 2;
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/note="assembly_name:Contig10
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nsucisei
Human protein tyrosine phosphatase receptor pi (PTPRP) mRNA,
complete cds.
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1 (bases 1 to 4699)
1 jiang, S., Tulloch, G., Fu, Y., London, R., Hummel, G.S., White, R.A., Avraham, H. and Avraham, S.
Characterization and chromosomal localization of PTPRP, a receptor protein tyrosine phosphatase predominantly expressed in brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
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2 (bases 1 to 4699)

Jiang,S., Tulloch,G., Fu,Y., London,R., Hummel,G.S., White,R.A.,
Jiang,S., Tulloch,G., Eu,Y., London,R., Hummel,G.S., White,R.A.,
Direct Submission
Submitted (10-DEC-1996) Genetics, The Children's Mercy Hospital,
2801 Wyandotte Ave., Kansas City, MO 64108, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         2222 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA
                                                                                                                                                                                                                                                                                                                                                                                                               120 ATTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTTCGGAAAAGAAATGATA
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                                                                                                                                                                                                                           Gaps
Kindsvogel, W., Jelinek, L.J., Sheppard, P.O., Hagopian, W.A., Lagasse, J. M.
Islet cell antiqen 1851
Patent: US 6627735-A 34 30-SEP-2003;
Location/Qualifiers
1. C.328
/organism="unknown"
                                                                                                                                                                                                                         5;
                                                                                                                                                                                  Score 426.4; DB 6; Length 2328;
Pred. No. 2.8e-95;
0; Mismatches 3; Indels 2;
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                                                                                                                                /mol_type="mRNA"
                                                                                                                                                                                      Query Match 93.7%;
Best Local Similarity 98.9%;
Matches 449; Conservative (
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Kindsvogel, W., Jelinek, L.J., Sheppard, P.O., Hagopian, W.A. and
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 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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Lagases.j.M.
Lagases.j.M.
Islet cell antigen 1851
Patent: US 6300093-A 34 09-OCT-2001;
Location/Qualifiers
1. 2328
/organism="unknown"
/mol_type="mRNA"
                                                                                                               2328 bp
US 6300093.
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US 6627735.
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AR404162
AR404162.1 GI:40152195
                                                                                                                   Sequence 34 from patent
AR369583
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Unclassified.
1 (bases 1 to 2328)
                                                                                                                                                                                                                                              Unclassified.
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University, 4444 Forest 7 (bases 1 to 190846)
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Waterston, R.H.
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6 (bases 1 to 190846)
Waterston, R.
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DSEDPSSTGDGARIHTLLKDLQRQPAEVRGLNGLELDGMAELMAGLMQGVDHGVARGS
PGRAALGESGQADGPKATLRGDSFPDDGVQDDDBLYQEVHRLSATLGGLLQDHGSR
LLDGALPFARFLDMERKKSEHPESSLSBETAGVENVKSQTYSKDLLGQQPHSEPGA
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GRRLVEDVARLLQVPSSAFADVEVLGPAVTFKVSANVQNVTTEDVEKATVDNKDKLEE
SSGHRLKEKLGSGLGGDPGADATAYQELCRQRMATRPPRFEGPHTSRISSVSSQFSD
GPIPSPSARSSAASWSEEPVQSNMDISTGHMILSYMEPHLKNNNRLEKEWBALCAYQA
EPNSSFVAQREENVPKNRSLAVLTYDHSRVLLKAENSHSDYINASPINDHDPRNPA
                                                                                                                                                                                                                                                                                                 /translation="MGPPLPLLLLLLLPPRVLPAAPSSVPRGRQLPGRLDGVFGRC
QKVPAMDFXKEVSPVALQRLSKVALQKLSGTGGTWQDDYTQYWNDQELADLPKTYLRR
PEASSPARPSKHSVGSERKYTREGGALANALRRHLPFLEDLSQAPASDVLARTHTAQ
DRPPAEGDDRFBESLITYVAHTSALTYPPGPRYQLREDLLPRTLGQLQPDBLSPKVDS
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HUSBHIWGEDPLVRGFYLKNLOTNETRTVTQPHFLSNYDRGVPSSSRGLLDFRRKVN
KCYRGRSCPTIVHCSDGAGRGTYVLIDMVLNKWAKGAKEIDIAATLEHLRDQRPGMV
QTKEQFEFALTAVAEEVNAILKALPQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4391 CTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAACCC 4332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4690 AATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGGTTTCT 4631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 TCATTTCGATTAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATAGC 181
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/product="protein tyrosine phosphatase receptor pi"
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Pred. No. 3.7e-95;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2185. .3006
/gene="PTPRP"
/note="encodes catalytic domain"
                                                                                                                     /tissue_type="brain; pancreas"
1. .4699
                                                                                                                                                                                                                                                                /protein_id="AAB68603.1"
/db_xref="GI;2351576"
                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                  /map="7q22-qter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1834. .1908
/gene="PTPRP"
                                                                                                                                                           /gene="PTPRP"
                                                                                                                                                                                                     gene="PTPRP"
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Best Local Similarity 99.1%;
Matches 448; Conservative
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                                                                                                                                            gene
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Homo sapisum Bukaroa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dasses I to 190846)

E. (Dasses I to 190846)

Hillier, M. W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wajle, K., Sekhon, W., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delehaunty, K.D., Miner, T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Miner, T.L., Nash, W.E., Courtney, L., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Stromy, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowicz-Reilly, A., Leonard, S., Rohlfing, T., Rock, S.M., Tin Wollam, A.M., Abbott, A., Minr, P., Maupin, R., Wessener, J.P., Wendl, M., Abbott, A., Minr, P., Maupin, S., Woldmann, P.E., Strowmatt, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woessner, J.P., Wendl, M., Abbott, A., Williams, D., Bedell, J.W., Spieth, J., Bierit, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Sldred, J., Williams, D., Bedell, J.A., March, E., Gillett, W., Zhou, Y., James, R., Phelpe, K., Iadanoto, S., Bubb, K., Simms, B., Levy, R., Chiedenning, J., Kaul, R., Kent, W. J., Furey, T.S., Baertsch, R.A., Brent, M.R., Kelbler, E., Flicek, P., Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Torrents, D., Chinwalla, A.T., Gish, W.R., Rebler, B., Chen, B.D., Waterston, R.H. and Wilson, R.K. The DNA sequence of human chromosome?
AC006372 19.0846 bp DNA linear PRI 31-JAN-2004
Homo sapiens BAC clone kPl1-331D5 from 7, complete sequence.
AC006372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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Hou,S., Small,J. and Wohldmann,P.
The sequence of Homo sapiens BAC clone RP11-331D5
Unpublished (2001)
3 (bases 1 to 190846)
Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov, or see http://genome.wustl.edu
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On May 5, 1999 this sequence version replaced gi:4139346.
                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J. J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACCe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the right is RP4-703PB. Actual start of this clone is at base position 1 of RP11-331D5 actual end is at
                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
                                                                                                                               Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                           Center project name: H NH0331D05
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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342. .476
/rpt_family="L1"
1730. .1793
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/rpt_family="Alu"
4686. 400r
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/rpt_family="Alu"
5406. .5577
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/rpt_family="Alu"
6534. .6809
/rpt_family="Alu"
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'rpt_family="Alu"
541. .3836
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6105. .6259
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rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="7"
                                                                                                              code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAPPING INFORMATION:
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                            COMMENT
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150838 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 150897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="VADDDALAEERWRRGGNALPAQPAGLRPPKPPRPASLLRHAPHC
LSEEEGGQDRPRAPGPWDPLASAAGLKEGGKRKKGKQREESKKKKSTKGNH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Homo sapiens, MRJ gene for a member of the DNaJ protein family, clone MGC:1152 IMAGE:3346070, mRNA, complete cds.; H.NH0311D05.11
This gene was based on gi(12803262)
Continues from H_TD2506A20.1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 CICTICAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA
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                                                                                                                                                            'Tpt family="Alu"
11946. 12180
170te="CpG island (%GC=63.8, o/e=0.80, #CpGs=20)"
12930. 13229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
21196. .25150
/note="cpg island (%GC=68.7, o/e=0.74, #CpGs=72)"
21514. .29158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
25960. .26373
/gene="DNAJB6"
/note="CpG_island (%GC=65.0, o/e=0.73, #CpGs=33)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CpG island (%GC=66.5, o/e=0.69, #CpGs=18)"
23786. .23910
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/gene≈"DNAJB6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9.2e-95;
0; Mismatches 4
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98.7%; Pred. No. 9.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(21514. .21720,27735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAS07521:1"
/db_xref="G1:41473761"
                                                                                                                         rpt_family="MER2_type"
1395. .11687
                                                                                                                                                                                                                                  /rpt_family="Alu"
13846. 13369
13946. 13369
13976. 14020
/rpt_family="MIR"
14625. 15183
/rpt_family="ERV1"
15184. 15385
/rpt_family="Alu"
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15699. .15992
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16004. .16221
/rpt_family="Alu"
16222. .16524
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25438. .25739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
6525. 16652
         rpt_family="Alu"
667. .7967
                                                   'rpt_family="Alu"
9590. .9745
                                                                                     rpt family="Alu"
1186. .11316
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Best Local Similarity
repeat_region
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: i Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19743910.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVMDQELADLEKTYLEREPEASSPARPSKHSVGSERRYSREGGAALANALRRHIPFLEA
LEGAPASDVLARTHTAQDREPAEGDENSESSITTYVAHTSADERTQLREDLLE
RITGOLQPDELS PKYVDGGVDRHILMAALSAYAAQREPAPPGGGSLERPQYLLRAPSRMP
RPLIAAPAAPQKWPSPLGDSEDPSSTGDGARIHTLIKDLQQPAEVRGLSGLELDGMAE
ILMGLMQGVDHGVARGSPGRAALGSEGGADGFARTLKGDESPPDGWQDDDBLYQEV
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TYSKDLLGQQPGSEGAAARGELQNQMIGPSKEEGQSLPAGAQBALSDGLOLEVQPSEE
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                                                                                      Genome
CA 94305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARGYIVTÖREVLGPAVTFKVSANVÕNVTTEDVEKATVDNKDKLEETSGLKILQTGVG
SKSKLKFLPPQAEQEDSTKFIALTLVSLACILGVLLASGLIVCLRHSSQHRLKEKLSG
LGGDPGADATAAVQELCRQRMATRPPDRPEGPHTSRISSVSSQFSDGPIPSPSARSSA
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ADFWQMVWESGCVVIVWLTPLAENGVRQCYHYWPDEGSNLYHIYEVNLVSEHIWCEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVRSFYLKNLQTNETRTVTQFHFLSWYDRGVPSSSRSLLDFRRKVNKCYRGRSCP11V
HCSDGAGRSGTYVLIDMVLNKMAKGAKEIDIAATLEHLRDQRPGMVQTKEQFEFALTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1656 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCGASEACVNDGVFGRCQKVPAMDFYRYEVSPVALQRLRVALQKLSGTGFTWQDDYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ATTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
Shiraki
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                         Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

CDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943

Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="PTPRN2"
/note="synonyms: IA-2beta, IAR, ICAAR, KIAA0387, PTPRP,
IAR PTPRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphatase, receptor type,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4716 GAAATCAGAAGTTTAATATGACACAATTAAATATATTGTATATATCTCACACCGGAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAATCAGAAGTTTAATATGACACAATTAAAATATATTTGTATATCTCACACCGGA-GNTT
DNA Library Preparation: Michael J. Brownstein (NHGRI) &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="protein tyrosine phosphats
polypeptide 2, isoform 3 precursor"
/protein id="AAH34040.1"
/db_xref="GI:21707839"
/db_xref="GI:21707839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.4%; Score 416; DB 9; Le
98.9%; Pred. No. 1.1e-92;
Migmatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="NHH MGC_95"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .4735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="LocusID:5799"
/db_xref="MIM:601698"
105_ :3065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="PTPRN2"
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Best Local Similarity
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Klausner, R.D., Colling, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Colling, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Carcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                   ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 150956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1317 CCCACACAGGAAATCTGCACCCACACAGGCTGCCTCTGTGCCGCCTTCCATGTGATCATC 151196
                                                                                                                                                                                                                                                                                                                                        151076
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 151136
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                                   ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 4735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens protein tyrosine phosphatase, receptor type, N polypeptide 2, transcript variant 3, mRNA (cDNA clone MGC:26506 BC034040
                                                                                                                                                                                            150957 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTGGCA
                                                                                                                                                                                                                                                                               TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCCTTTGGAGGAGTACCATCT
                                                                                                                                                                                                                                                                                                                                     151017 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT
                                                                                                                                                                                                                                                                                                                                                                                                     ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAAC
                                                                                                                                                      GCTATATAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: hiklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151197 TTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 151230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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Direct Submission
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VERSION
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ORGANISM
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REFERENCE
AUTHORS
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JOURNAL
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COMMENT
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CILGVLIASGLIYCLRHSSQHRLKEKLSGLGGDPGADATAAYQELCRQRMATRPDRP
BGPHTSRISSVSSQFSDGPIPSPSARSSASSWSEEPVQSNMDISTGHMILSYMEDHLK
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GVPSSGRSLLDPRRKVNKCYRGRSCPIIVHCSDGAGRSGTYVLIDMYLNKAAKGAKEI
DIAATLEHLRDQRPGWVQTKEQFFFALTAVAEBVNAILKALPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1996
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
                                                                                                                                                                                                                                                                                                                 GAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGGTTTCTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4351 AGGAAATCTGCAGCCCCACACAGCTGCCTCTGCGCCCTTCCATGTGATCATCTGCTGCTGGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 TCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATAGTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4590 TCGATTAATTAAATTCCAGATAAAGAGAAGTAATTTT-GGAAAAGAAATGATAGCTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 AGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCGCCTTCCATGTGATCATCCTGGTCA
                                                                                                                                                                                                                                                                                          8 GAAGTITAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTTCTCTTCA
                                                                                                                                                                                                                                                                                                                                                                               67 AACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATT
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                                                                                                                                                                                                    91.1%; Score 414.6; DB 9; Length 98.2%; Pred. No. 2.5e-92; ive 0; Mismatches 6; Indels
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G19707
G19707.1 G1:1340278
STS; STS sequence; primer; sequence tagged site.
Home sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96C 5min
54C 30sec
72C 30sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4291 ATGAAGTGAGTTGTCCTATTTCGGGGG 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer A: ACAATACCATGAGAGACATAAG
Primer B: ATCTTAGATAGATGGTACTCTCC
STS size: 105
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 ATGAAGTGAATTGTCCTATTTCNGGGG 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anneal:
Extend:
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                                                                                                                                                                                                                             al Similarity 98.2
439; Conservative
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Best Local S
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LMAGLMQGVDHGVARGSPGRAALGESGEQADGPKATIRGDSPPDDGYQDDDDRLYQEV
HRLSATLGGLLODHGSRILPGALPFARPLDMERKKSEHPESSLSSEESTAGVENVKSQ
YSKDLLGQQPHSEPGAARLQNQWPGPSKERQSLPAGAQBALSGLLOVPSEE
BARGYIYTDRDPLRPEGRRIVGDAYALLQVPSSAFADVEVLGPAYFKVSAWONY
TEDVEKATVDNKOKLEETSGLKILLQYGGSKSKLKFLPPQAEQEDSTKFIALTUVSLA
                                                                                                                  4478
                                                                                                                                                                                                        4419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein id="AAC50742.1"
/db_xref="GI:1620664"
/translation="MGPPLPLLLLLLLLLPPRVLPAAPSSVPRGRQLPGRLGCLLEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCGASEACVNDGVFGRCQKVPAMDFYRYEVSPVALQRLRVALQKLSGTGFTWQDDYTQ
YVMODELADLENTYLRRPEASSPARBSKHSVGSBRRYSREGGAALANALRRHLPFLEA
LSQAPASDVLARTHTAQDREGDDRFSESILTYVANTSALTYPPGRRTQLREDLLD
RTLGQLQPDELSPKVDSGVDRHLIMAALSAYAAQRRPPAPGGSGSLEPQYLLRAPSRMP
                             ATTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTT-GGAAAAGAAATGATA 4538
                                                                                                                                                                                                                                                                                          4418 ATCTAAGATGGAGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 4359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-AUG-1996) Barbara Davis Center for Childhood Diabetes, University of Colorado Health Sciences Center, 4200 East 9th Avenue, Box B-140, Denver, CO 80262, USA Location/Qualifiers
                                                                         239
                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                    300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGGGGGATGGAGGTGCGTTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawasaki, E., Hutton, J.C. and Eisenbarth, G.S.
Molecular cloning and characterization of the human transmembrane
protein tyrosine phosphatase homologue, phogrin, an autoantigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                         GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTGGCA
                                                                                                    TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGGAGTACCATCT
                                                                                                                                                                                                        4477 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTT-GAGAGTACCATCT
                                                                                                                                                                                                                                                                                                                                        CCCACACAGGAAATCTGCAGCCCACACAGCTGCGCTCTGCGCCGCCTTCCATGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 4719)
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Kawasaki,E., Hutton,J.C. and Eisenbarth,G.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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/organism="Homo sapiens"
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Human phogrin mRNA, complete cds.
U66702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="islet"
/tissue_type="pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="phogrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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(bases 1 to 180187)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-366B11, *** SEQUENCING IN PROGRESS AC117965
                                                                                                                                                                                                                                                                                                                                                                                                                     Prepared with primer pairs derived from THC51137; GenBank Accession Numbers-- F09140, F10434, T03688, T15930, T19338, T32236, T33356,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 ACAATACCATGTAGAGACATAAGCAATATTTTGGCATCATTCTGTCCGCTCAGTAGGCCG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAATACCATGTAGAGACATAAGCAATATTTTTGGCATCATTCTGTCGGTCAGTAGGCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.1%; Score 105; DB 11; Length 10
100.0%; Pred. No. 1.6e-15;
tive 0; Mismatches 0; Indels
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Rattus norvegicus (Norway rat)
                                                                                        25 ng
0.43 uM each
230 uM each
95C 30sec
72C 5min
30
                                                                                                                                                            Amplifaq: 0.5 units
FaqStart Ab: 0.5 units
Total Volume: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .105
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                          Tris-HCl pH8.8: 100 mM
KCl: 500 mM
MqCl2: 20 mM
                                                                                                                                                                                                                                                                                                                        MgCl2: 20
Triton X-100: 1%
Concentration: 10X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (83. .105)
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  Denature:
FinalExtend:
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                                                                                           GenomicDNA:
                                                Cycles:
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Best Local Similarity 100.0
Matches 105; Conservative
                                                                                                                   Primer:
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T33873.
                                                                     Protocol:
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AC117965/c
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hennandez, J., Jang, H., Johnson, R., Johnson, R., Jackson, J., Jackson, L., Jacob, H., Johnson, B., Johnson, R., Lou, J., Liu, Y., Loulesged, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., Loulesged, H., Lozado, R.J., Lu, X., Man, M., Mahindartne, M., Mahmoud, M., Marloy, K., Mangum, A., Mangum, B., Mayua, P., Martin, K., Martinez, E., Mangum, R., Mangum, P., Martin, R., Martin, R., Mangum, P., Martin, R., Martin, R., Martin, R., Mangum, P., Mangum, P., McLeod, M.P., McNeill, T.Z., Menen, E., Morgan, M., Moris, K., Mortis, S., Munidasa, M., Murit, S., Parks, K., Norden, R., S., Parks, R., Nordelem, D., Okucon, G., Olarnpunesgoon, A., Pal, S., Parks, K., Pasternak, S., Panks, R., Pold, H., Perez, A., Peisz, L., Peiankoch, C., Smal, D., Newton, N., Nguyen, N., Norris, S., Nunderlem, R., Sold, H., Rose, M., Rose, R., Ruiz, S.J., Shen, H., Steen, C., Shen, Steinle, M., Steong, R., Sutteon, E., Soctt, G., Shatsman, S., Shen, Steinle, M., Steong, R., Stutton, A., Stason, I., Sitter, C.D., Smajs, J., Steinle, M., Stong, R., Sutton, A., Stason, I., Steter, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Weinler, R., Wang, S., Warten, R., Weis, X., Millams, G., Wang, S., Warten, M., Warten, R., Weis, X., Millams, G., Willams, D., Warten, R., Weish, X., Weish, K., Weish, K., Weish, W., Weish, K., Weish, K., Weish, K., Weish, W., Weish, K., Direct Submission

Submitted (20-00V-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23811557.

The sequence in this assembly is a combination of BAC based reads and whole genome shocton sequencing reads assembled using Arlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Arlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shocton sequence reads. Both end sequences and whole genome shocton sequence reads. Both end sequences and whole genome table. Worley, K.C.
Direct Submission
Submitted (12-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 180187)
Rat Genome Sequencing Consortium. Center flor name: CH230-366B11
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 169631 bases at least Q40
Consensus quality: 171486 bases at least Q30 Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Center project Information

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112. .3126
/gene="PTPNE6"
                                                                                                                                                                                                                                                                                                    gene="PTPNE6"
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                                         9109506
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AUTHORS
TITLE
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AC110936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163089 CATAAGAAG-----TTACAATTAAGTATATGCTTCCTATATTCAGATAAATTCATTTC 163037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163036 TATTAATTATCATTTAGATTCCGGGAAGGGGGAAATGGAAGGGAACG-TCGCAGATGTT 162978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus protein tyrosine phosphatase (PTPNE6) mRNA, complete cds.
                                                                          NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 CATAAGGAGTIAGAAATTACAAGTAGGCATAIGCTTCCTATATTCAGATAAATTCATTTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATAGCTATATTA 188
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGNTTCTCTTCAAA 68
Consensus quality: 172615 bases at least Q20
Estimated insert size: 175046; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus.

1 (bases 1 to 5136)
Fitzgerald,L.R., Walton,K.M., Dixon,J.E. and Largent,B.L.
PTP NE-6: a brain-enriched receptor-type protein tyrosine
phosphatase with a divergent catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 18.9%; Score 86.2; DB 2; Length 180187; Local Similarity 71.5%; Pred. No. 1.2e-10; nes 143; Conservative 0; Mismatches 49; Indels 8;
                                                                                                                                                                                                                                                                             1 178750: contig of 178750 bp in length 178751 178850: gap of unknown length 178851 180187: contig of 1337 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end_sequence:B2121917"
176880. .178750
/note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172128. 173041
/note="clone_boundary
clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CH230-366B11"
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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note="wgs_contig"
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RNU73458/c
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2 (bases 1 to 5136)
Pitzgerald, D.R., Walton, K.M., Dixon, J.E. and Largent, B.L..
Direct Submission
Submitted (04-007-1996) CNS Diseases Research, DuPont Merck
Research Labs, Experimental Station E400, Wilmington, DE 19880, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACLIU936 222251 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-188N19, *** SEQUENCING IN PROGRESS
***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPRNPAYIATGGPLPATVADFWGMVWESGCAVIVMLTPLSENGVRQCHHYWPDEGSNV
YYYZEVNLVSEHIWQDFLVNSFYLLWGLQTNETTVTQFHFLSWYDQSVPSSTRSLLD
FRRKVNKCYRGRSCPIIVHCSDGAGRSGTYVLIDMVLNKMAKGAKEIDIAATLEHLRD
QRPGWYQTKEQFEFALTAVAEEVNAILKALPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4567 AGGITIAATAGGACACAATIAAATATATCIGTATATCACACCGAGGGTTTTTCCTTTAAA 4508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4454 TATTAATTATCATTTAGATTCCGGGAAGGGGGAAATGGAAGAGGAACGTCGCAGATGTTA 4395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85.6; DB 10; Length 5136;
Pred. No. 1.4e-10;
0; Mismatches 45; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="protein tyrosine phosphatase"
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AC110936
AC110936.6 GI:25072900
HTG; HTGS PHASE1; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprsgue-Dawley"
/db_xref="taxon:10116"
Neurochem. 68 (5), 1820-1829 (1997)
                                                                                                                                                                                                                                                                                                                                                                                            function="receptor-type"
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us-08-731-499-8.rge

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misc_feature
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                                                                                                                                            Hearse, Louise, Abramicon, S., Adame, C., Alder, J., Anjahan, D., Marie, M., Merzker, M. Lee., Abramacon, S., Anjabrocks, S., Amin, M., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balabrocks, S., Amin, M., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baladrin, D., Bandarnalke, D., Barbare, M., Barnated, B., Barbare, M., Baladrin, D., Bandarnalke, D., Barbare, M., Barnated, B., Brown, M., Biswalo, K., Blart, J., Blankenburg, K., Blyth, P., Brown, M., Carter, K., Cavazo, D., Ceap, M., Cree, D., D'Gouza, L., Davila, M., Care, D., Corkell, R., Chen, S., Chan, C., Coye, D., Danson, S., Deramo, C., Coye, D., Danson, S., Deramo, C., Ding, Y., Dunh, H., Davya, K., Danshad, C., Denson, S., Deramo, C., Ding, Y., Dunh, H., Davya, K., Danshade, S., Fally, M., Capisi, A., Garte, M., Garis, M., Ganis, R., Garte, M., Garte, M., Ganis, R., Garte, M., Garte, M., Ganis, R., Garte, M., Garte, M., Ganis, R., Hander, M., Handlon, S., Hander, M., Harnandez, S., Fillys, M., Fallys, M., Fallys, M., Fallys, M., Hander, M., Hander, M., Handlon, S.L., Hodgeon, A., Harnandez, M., Hander, S., Hulys, S., Kallys, K., Kati, L., Li, L., Li, Li, J., Liu, J., Liu, W., Liu, Y., London, P., London, P., London, P., London, P., London, P., London, P., London, R., Mandoud, M., Maland, M., Maland, M., Martin, M., Mahmedwari, M., Moris, S., McLeod, M. P., Martin, R., Martin, R., Martin, M., Martin, W., Martin, M., Martin, M.,
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ON NOV 19, 2002 this sequence version replaced gi:23270153.
The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rat Genome Sequencing Consortium.
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Worley, K.C.
                                                                                                                                     (bases 1 to 222251)
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ORGANISM
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JOURNAL
                                                                                                                                                                 AUTHORS
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COMMENT

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127895 AGGTTTAATAGGACACAATTAAATATATCTGTATATCACACCGAGGGTTTTTCCTTTAAA 127954
                            individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center Clohe name: CH230-188N19
------ Summary Statistics
Assembly program: Phrap; versus of 1990329
Consensus quality: 193700 bases at least Q40
Consensus quality: 195702 bases at least Q30
Consensus quality: 186702 bases at least Q30
Consensus quality: 186702 bases at least Q30
Consinered insert size: 196105; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AAGTITAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGNTTCTCTTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.9%; Score 76.8; DB 2; Length 222251; Best Local Similarity 80.6%; Pred. No. 2.7e-08; Matches 104; Conservative 0; Mismatches 18; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213437: contig of 213437 bp in length 213537: gap of unknown length 218989: contig of 5452 bp in length 219089: gap of unknown length 220060: contig of 1517 bp in length 220760: gap of unknown length 22051: contig of 1491 bp in length.
                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                   College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                       Center project Information
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/db_xref="taxon:10116"
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27659. .28735
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213538. .215409
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[6434. .18286
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128775. .130020
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[74053. .175360
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83232. .184558
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Search completed: May 5, 2005, 03:58:33 Job time : 2231.09 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aav09022 Homo sapi	Aah34753 Human col	Aat9527 Human isl	Add14680 Human src	Adn95437 Human BEC	Adp18660 Human TAT	Abv95893 Human pan	Aas87633 DNA encod	Adf86738 Single nu	Adf86737 Single nu	Adf86735 Single nu	Adf86734 Single nu	Adf86736 Single nu	Aah35240 Human col	Adq53174 Novel can	Aal29285 Human SNP	Ada71938 Rice gene	Abl34540 Human met	Abl70263 Chemicall	Ads99801 Bisulphit
SUMMARIES	ID	AAV09022	AAH34753	AAT95227	ADD14680	ADN95437	ADP18660	ABV95893	AAS87633	ADF86738	ADF86737	ADF86735	ADF86734	ADF86736	AAH35240	ADQ53174	AAL29285	ADA71938	ABL34540	ABL70263	ADS99801
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æ	Query Match	9.66	96.5	93.7	93.6	93.6	91.1	26.0	49.5	26.5	25.2	24.1	23.6	20.4	14.2	12.0	10.9	10.0	7.6	7.6	9.7
	Score	453	439	426.4	426	426	414.6	254.8	225.2	120.6	114.6	109.6	107.6	92.6	64.4	54.6	49.4	45.4	44.2	44.2	44.2
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The sequence is that of a cDNA sequence 20sa7 which was isolated from the 20q13 amplicon. It is a homologue of the rat gene BEM-1 and can be used as a probe for the detection of chromosomal abnormalities at 20q13. It and other sequences isolated from the 20q13 amplicon are consistently

New sequences from the 20q13 amplicon – used for detecting chromosomal abnormalities, particularly tumours, and for developing products for treating diseases.

Claim 1; Page 63-64; 91pp; English.

Abk39937 Human che	Abl32219 Human imm	Abq66997 Human ang	Ada71938 Rice gene	Aaz42154 Human nor	Aat61258 560E1 cDN	Aaf21830 Human bre	Adr67210 Human bla	Adr66257 Human pro	Adr66599 Human pro	Aas46787 Tumour su	Aal29288 Human SNP	Aah93307 Plasmodiu	Aal29282 Human SNP	Aaf12929 Aspergill			Abl14726 Drosophil	Continuation (10 o			Abq42952 Oligonucl	Abq42953 Oligonucl	Ado55043 Gene #140	Aah93026 Human inf
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9.7	9.7	9.7	9.7	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.4	9.4	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.0	8.0	8.9	8.9	8.9
44.2	44.2	44.2	44	43	43	43	43	43	43	43	42.6	42.6	42	42	42	42	41.6	41.4	41.2	41	40.6	40.6	40.4	40.4
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

20q13 amplicon; chromosome 20; tumour; detection; chromosomal abnormalities; probe; gene therapy; antisense inhibition; treatment; age-related macular degeneration; retinitis pigmentation; Leber's congenital amaurosis; BEM-1; ds. Rommens J; Kowbel D, Homo sapiens 20q13 amplicon 20sa7 transcript. Godfrey T, Gray JW, Collins CC, Hwang S, BP. 96US-00680395. 96US-00731499. 97US-00785532. AAV09022 standard; cDNA; 455 97WO-US012343 (first entry) (REGC) UNIV CALIFORNIA. WPI; 1998-110587/10. WO9802539-A1. 15-JUL-1996; 16-OCT-1996; 17-JAN-1997; Homo sapiens. 15-JUL-1997; 21-JUL-1998 22-JAN-1998. AAV09022; RESULT 1 AAV09022

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amplified in primary tumours. These sequences are useful as probes or as probe targets for monitoring the relative copy number of corresponding sequences from a biological sample such as tumour cells. The sequences can also be used in therapeutic applications for modulating the expression of the endogenous gene or the activity of the gene product. Examples of therapeutic approaches include antisense inhibition of gene expression, gene therapy, and monolonal antibodies that specifically bind the gene products. The products can also be used in the treatment of other diseases, e.g. age-related macular degeneration, Leber's congenital amaurosis and retinitis pigmentation
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                                                                                                                                                                                                                         Length 455;
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                                                                                                                                                                                        Sequence 455 BP; 138 A; 87 C; 98 G; 130 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen encoding cDNA SEQ ID NO:1835.
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                                                                                                                                                                                                                        99.6%; Score 453; DB 2;
100.0%; Pred. No. 5e-118;
iive 0; Mismatches 0;
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Best Local Similarity
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03-NOV-1999;
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis of cancer the categories of dispression by rectifying mutations or deletions in a patient's genome example. N and P may be used to treat disporters associated with decreased complement the patients own production of P. Additionally. N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37789 represent

Sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1093 TTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1213 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1153 TCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 96.5%; Score 439; DB 4; Length 12
Best Local Similarity 99.3%; Pred. No. 6.9e-114;
Matches 450; Conservative 0; Mismatches 2; Indels
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                                                              Rosen CA;
                                                                                                                                                                                                                                    Claim 1; Page 3372-3373; 9803pp; English.
                                                                Birse CE,
                      HUMA-) HUMAN GENOME SCI INC
                                                                Barash SC,
                                                                                                          WPI: 2001-235357/24
                                                                                                                              P-PSDB; AAG75348
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                                                                Ruben SM,
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RESULT 3 AAT95227/c

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1983 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 1924
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                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence comprises clone WK121315 a partial cDNA clone of novel human islet cell antigen 1851. It was isolated from human insulinoma cDNA by PCR amplification (see AAF9524-25). Other partial clones (see AAF95226 and AAF95228) were similarly obtained. Subsequent 5' RACE yielded a claimed sequence (see AAF95221) for islet cell antigen 1851 (see AAM95297). This antigen forms an immun complex with an altocantibody found in patients at risk of corporations.
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                                                                                        Islet cell antigen 1851; autoantigen; protein tyrosine phosphatase;
insulin-dependent diabetes mellitus; IDDM; diagnosis; therapy; human; ds.
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                                                                                                                                                                                                                                                                                                                                    - used to detect
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auto:antibodies indicative of insulin-dependent diabetes or pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 426.4; DB 2; Length 2328;
Pred. No. 3.3e-110;
); Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                        Lagasse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2328 BP; 597 A; 599 C; 595 G; 537 T; 0 U; 0 Other;
                                                                  Human islet cell antigen 1851 partial cDNA clone WK121315.
                                                                                                                                                                                                                                                                                       Sheppard PO, Hagopian W,
                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 114-115; 134pp; English.
 AAT95227 standard; cDNA; 2328 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.7%;
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                                                                                                                                                                                                                                                                                      Kindsvogel W, Jelinek L,
                                            (first entry)
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Best Local Similarity 98.9
Matches 449; Conservative
                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                            disposition to it.
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                                             27-MAR-1998
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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase contains the activity of cells, comprising obtaining a sample of cells, correlating the expression of the markers a plurality of markers, and correlating the expression of the markers a plurality of markers, and correlate the activity of the cells; (2) a plurality of cells lines for identifying polynucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynucleotides and cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polynucleotides or polypeptides, and selecting coll lines to one or more compounds, analysing the expression pattern of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides are useful in predicting the coll public protein tyrosine kinases and/or activity of compounds that interact with protein tyrosine kinases and/or activity of compounds that interact with protein tyrosine kinases and/or activity of compounds that interact with protein tyrosine kinases and/or activity of compounds that interact with protein tyrosine kinases and/or activity of compounds that interact with protein expression pattern of the microarray of activities and polypeptides are useful in predicting the content of the microarray of the protein kinases and polypeptides and polypeptides are useful in predicting the content of th
                                                                predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
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CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                                                                                                                         1863 CIGGICAAIGAAGIGAAITGICCIATITICIGGGG 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human src biomarker polynucleotide SEQ ID NO:74.
                                                                                                                                                                                                                         453
                                                                                                                                                                                                                         CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG
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P-PSDB; ADD14084.
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                                                                                                                                                                                                                                                                                                                                                                                              CACACAGGAAATCTGCAGCCCCACACAGCTGCCTCTGCGCCCTTCCATGTGATCATCCT 4272
                                                                                                                           4690 AATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGGTTTCT 4631
                                                                                                                                                                        4630 CTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAAT 4571
                                                                                                                                                                                                                    4570 TCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTT-GGAAAAGAAATGATAGC 4512
                                                                                                                                                  121
                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                      ATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCTAT 301
                                                                                                                                                                                                                                                                                                                                    CTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAACCC 361
                                                                                                                                                                                                                                                                                                                                                                                 CACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATCCT 421
                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth, differentiation, blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cycostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
                                                                                                                                                  CTTCAAACATAAGGAGTTAGAAATTACAAGTAGCCATATGCTTCCTATATTCAGATAAAT
                                                                                                                                                                                                                                         182 TATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAAGCAATATTTTGGCATC
                                                                                                     3 AATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTTCT
                                                                               Gaps
cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saharinen P, Saharinen J;
                                 Sequence 4699 BP; 1058 A; 1402 C; 1328 G; 911 T; 0 U; 0 Other;
                                                                              Indels
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7
                                                      Score 426; DB 10;
Pred. No. 5.6e-110;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BEC/LEC-related gene sequence SeqID360.
                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCAATGAAGTGAATTGTCCTATTTCNGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4271 GGTCAATGAAGTGAATTGTCCTATTTCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN95437 standard; DNA; 4767 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
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                                                      Query Match 93.6%;
Best Local Similarity 99.1%;
Matches 448; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2002; 2002US-0363019P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003080640-A1
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises contaction and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation in at least one allele of a gene encoding a LEC protein, where the mutation in at composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the becompounds with an antiangiogenic, cytostatic, composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphocdema, in screening for an endothelial cells, in treating hereditary cycle advisement for the discorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the treatment of the discorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a cell or lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting the supparation. The lymphatic growth agent may also be used in manufacturing a wedicament for the treatment of hereditary lymphoedema resulting the lymphatic system or of other diseases and cancer metastasis via the lymphatic constructions inflammatory diseases and cancer metastasis via the lymphatic system. The presents sequence is that of a human LEC and the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1638 TCATTTCGATTAATTAAATTCCAGATAGAGAAAGTAATTTT-GGAAAAGAAATGATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 TATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 ATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4767 BP; 1065 A; 1426 C; 1354 G; 922 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4767;
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                                                                                                                                     Example 1; SEQ ID NO 360; 176pp; English.
    2003-876899/81
WPI; 2003-876899
P-PSDB; ADN95436
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4308 453

GGTCAATGAAGTGAATTGTCCTATTTCNGGGG

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WO200260317-A2.
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247
                                                                                                                                                                                                                                                                                                                                    ABV95893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4710 GAAGTTTAATATGACACAATTAAATATTTTGTATATCTCACACCGGAGGTTTCTCTTCA 4651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATAGCTATAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody that binds to tumor-associated antigenic target polypeptide (TAT), useful in preparing a composition for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to novel isolated antibodies that are useful for the diagnosis and treatment of a tumour. Specifically, it refers to DNA that is detectably labelled and conjugated to a growth inhibitory or cytotoxic agent and comprises toxins, antibiotics, radioactive isotopes or nucleolytic enzymes. The present invention refers to the toxin maytansinoid or callcheamicin, where the host cell is one of chinese hamster overy (CHO), yeast or Escherichia coli cell is one of chinese pharmaceutical compositions are cytostatic and can be used for gene therapy purposes to treat various cancers. This polynucleotide sequence
                                                                                                                                                      tumour; growth inhibitory; cytotoxic; cytostatic; gene therapy; cancer;
human; TAT; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTTCTCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 414.6; DB 12; Length 4719; 98.2%; Pred. No. 9.6e-107; ative 0; Mismatches 6; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4719 BP; 1057 A; 1404 C; 1340 G; 918 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonzalez L,
), Zhang Z;
                                                                                                                                         Human TAT418 cDNA used to treat cancer SegID 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy purposes to treat various cancers. Thi
is a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Frantz G, Goddard A, Goi
Polakis P, Polson A, Wood WI, Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 20; 183pp; English.
           RESULT 6
ADP18660/c
ID ADP18660 standard; cDNA; 4719 BP.
                                                                                                                                                                                                                                                                                                                  13-NOV-2003; 2003WO-US036298.
                                                                                                                                                                                                                                                                                                                                                     15-NOV-2002; 2002US-0426847P.
                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2002; 2002US-0431250P.
                                                                                                           (first entry)
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Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-420515/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADP18681.
                                                                                                                                                                                                                                                      WO2004045516-A2.
                                                                                                                                                                                                                        Homo sapiens
                                                                                                           26-AUG-2004
                                                                                                                                                                                                                                                                                      03-JUN-2004
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                                                                            ADP18660;
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TAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCATCATTCT

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The invention relates to an isolated polynuclectide (I) comprising: (a) any of a group of over 4000 nuclectide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of a Least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pencreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and pancreatic tumor polypeptides, useful f
diagnosing, preventing and/or treating cancer, particularly pancreatic
cancer.
4411 ATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTATACGCTGAACCCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1301; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                Human pancreatic cancer expressed cDNA SEQ ID NO 1301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Persing DH,
                                                                                                                                                                                               ATGAAGTGAATTGTCCTATTTCNGGGG 453
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                                                                                                                                                                                                                                                                                     ABV95893/c
ID ABV95893 standard; cDNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001US-0265305P.
31-JAN-2001; 2001US-0265682P.
09-FEB-2001; 2001US-0267568P.
21-MAR-2001; 2001US-0278651P.
28-APR-2001; 2001US-0287112P.
16-MAY-2001; 2001US-03131P.
12-JUL-2001; 2001US-0305484P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; tumour; gene; BB.
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-627435/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to tract disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to a ssesse biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1653 TAGCTATATTAAAGGCAGGATATTCATTACAATACCATGTAGAGACATACGGCAATATTA 4594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4773 CTCTTCAAACATAAGGATTTATCAAATTACAAGTAGGCATATGCTTCCTATATTCAGATA 4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTTCTACGCTGAACCCCACACA - GGAAATCTGCAGCCCACACAGC-TGCCTCTGCGC 400
                                                                                                                                                                                                                                                            coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGGCATCATICIGICCGCT----CAGIAGGCCGIGITCCCTCTGGTAGGGCC---TITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4713 AATTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTGGGAAAAGCAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTTCAAACATAAGGAGTTA-GAAATTACAAGTAGGCATATGCTTCCTATATTCAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTCATTTCGATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAG-AAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCTATATTAAAG--CAGATATTCATTACAATACCATGTAGAGACATAAG--CAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAAATCAGAAGTTTAATATGACACAATTAAATATTTTGTATATCTCACCGG-AGNTT
                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 4856;
                                                                                                                                                                                                                                                                                                                                                   Sequence 4856 BP; 1082 A; 1454 C; 1374 G; 946 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                     ttch 49.5%; Score 225.2; DB 5; sal Similarity 82.4%; Pred. No. 4.4e-53; 394; Conservative 0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                   tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF86738 standard; DNA; 121
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Matches
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     polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                         ATTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATAGCTATAATAA
                                                                                                                                                                                                                                                                                                                                                                                           ATTAATTAAATTCCAGATAAAGAGAAGTAATTTT-GGAAAAGAAATGATAGCTATATTAA
                                                                                                                                                                                                                                70 ATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCG
                                                                                                                                                                                                                                                                                                                     ATAAGTAGTIAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCATCATTCTGTC
                                                                                                                                                                                                           11 GTTTAATATGACACAATTAAATATATTGTATATATCTCACACCGGA-GNTTCTCTTCAAAC
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide and encoded polypeptides, useful in
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                                                                                                                                56.0%; Score 254.8; DB 6; Length 282; 98.2%; Pred. No. 5.8e-62; ive 0, Mismatches 3; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGT 1
                                                                                                BP; 92 A; 49 C; 44 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel human diagnostic protein #23437.
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AAS87633 standard; cDNA; 4856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                        278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
                                                                                                                                                     Best Local Similarity
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                                                                                                Sequence 282
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dB. 401. CGCCTTCCATGTGATCATCCT----GGTCAATGAAGTGAATTGTCCTATTTCNGGGGG 454 human; single nucleotide polymorphism; microarray; side effect; gene; CGGCCTTTCCATGGTGATCATCCTGGGTCAATGAAGTGAATTTGTCTGGGG SEQ ID No 321

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(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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                                                                                                                                                                                        The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 915 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligomorbidic containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YGCTGAACCCCACACAGAAATCTGCAGCCCACACACACGCTGCCTCTGCGCCCTTCCATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 CGCTGAACCCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCTTCCATG 411
                                                                                                                               Novel polynucleotide useful for detecting single nucleotide polymorphisms
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                                                                                                                                                                                                                                                                                                 polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the 935 isolated polymucleotides from a human gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 TACCATCTATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 120.6; DB 10; Length 121; Pred. No. 4.4e-24; 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121 BP; 27 A; 33 C; 34 G; 26 T; 0 U; 1 Other;
                                                                                                                                                                    Claim 1; SEQ ID NO 321; 704pp; Japanese.
                                                                                   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF86737 standard; DNA; 121 BP
                                                                                                                                                                                                                                                                                                                                                                                                             26.5%;
99.2%;
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                                  12-FEB-2002; 2002JP-00034717.
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                                                           12-FEB-2002; 2002JP-00034717
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                                                                                                          4PI; 2003-820454/77.
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                                                                                                                                            in human gene
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            26-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                  polynucleotide useful for detecting single nucleotide polymorphisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 BP; 25 A; 34 C; 30 G; 31 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.2%; Score 114.6; DB 1098.3%; Pred. No. 2.2e-22; iive 1; Mismatches 1
                                                                                                                                                                         Claim 1; SEQ ID NO 320; 704pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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WPI; 2003-820454/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                       in human gene
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ID ADF8
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in specification, or a sequence having a base substitution. The invention further relates to: an oligomucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo; proportion is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also useful for the isolated human gene. This polymorphisms in a human gene. This polymorleotide sequence represents one of the 935 isolated polymucleotides from a human gene of the
                                                                                                                                                                                                                                                                                                                                                                            invention
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149 GAGAGAAGTAATTTTCGGAAAAGAATGATAGCTATATTAAAGCAGATATTCATTACAAT 208 61 RAGAGAAGTAATTTT-GGAAAAGAAATGATAGCTATATTAAAGCAGATATTCATTACAAT 119 Score 109.6; DB 10; Length 121; Pred. No. 5.7e-21; 1; Mismatches 0; Indels 1; 1; Mismatches 24.1%; 98.4%; 120; Conservative Local Similarity Query Match Matches

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Sequence 121 BP; 50 A; 14 C; 17 G; 39 T; 0 U; 1 Other;

148

Gaps

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209 AC 210 AC 121 120 ò ద

ADF86734 standard; DNA; 121 (first entry) 26-FEB-2004 ADF86734;

Single nucleotide polymorphism detection human gene, SEQ ID No 317.

human; single nucleotide polymorphism; microarray; side effect; gene;

Homo sapiens

JP2003235571-A.

26-AUG-2003

12-FEB-2002; 2002JP-00034717

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

12-FEB-2002; 2002JP-00034717

WPI; 2003-820454/77

Novel

Claim 1; SEQ ID NO 317; 704pp; Japanese. human gene

polynucleotide useful for detecting single nucleotide polymorphisms

The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonocleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo, and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide

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134
                                                                                                                                                                                                                                                                                                                                                      61 KAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCGATTAA 120
polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymoclaoliide sequence represents one of the 935 isolated polymucleotides from a human gene of the
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                                                                                                                                                                                                                                                                                                                                  GAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCGATTAA
                                                                                                                                                                                                                                                          16 ATATGACACAATTAAATTTTGTATATCTCACACCGGA-GNTTCTCTTCAAACATAAG
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                                                                                                                                                                            DB 10; Length 121;
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                                                                                                                                        Sequence 121 BP; 44 A; 19 C; 15 G; 42 T; 0 U; 1 Other;
                                                                                                                                                                            Score 107.6; DB 1
Pred. No. 2.1e-20;
                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                            23.6%;
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ADF86736 standard; DNA; 121 (first entry) 26-FEB-2004 ADF86736; ADF86736

human; single nucleotide polymorphism; microarray; side effect; gene; ds. Single nucleotide polymorphism detection human gene, SEQ ID No 319

JP2003235571-A.

26-AUG-2003

dв.

12-FEB-2002; 2002JP-00034717.

12-FEB-2002; 2002JP-00034717.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2003-820454/77

polynucleotide useful for detecting single nucleotide polymorphisms human gene Novel Ξ

Claim 1; SEQ ID NO 319; 704pp; Japanese

The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing the SNP containing oligo; and gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymorphisms sin a human gene. This polymorphisms of the 935 isolated polymucleotides from a human gene of the invention 90.5%;

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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy cand vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased cypression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent C Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
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                                                                                                            419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                      1 CCCACACAGGAAATCTGCCACCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
                                                                                                          360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTTGCGCCGCCTTCCATGTGATCATC
                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; ss.
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                                      Length 121;
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                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen encoding cDNA SEQ ID NO:2322.
Sequence 121 BP; 26 A; 33 C; 32 G; 29 T; 0 U; 1 Other;
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                                      DB 10;
                                  20.4%; Score 92.6; DB 10, 97.9%; Pred. No. 3.7e-16; ative 1; Mismatches 1,
                                                                                                                                                                                  420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
                                                                                                                                                                                                     61 YTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 94
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                                                     Best Local Similarity 97.9
Matches 92; Conservative
                                  Query Match
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14.2%; Score 64.4; DB 4; Length 455;

Query Match

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in the interior of the construction of canine microarrays containing a sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic caid sequences of the invention may be useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that condulate gene expression or activity. The database is useful for producing electronic Northernus that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a samilarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the similarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the liver liver necrosis, fatty liver cannot brain or testes, or other pathologies associated with at least one
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                                                                                             147 AAATCAGAAGTTTAATATGAGNCAATTAAATATATTTGTATATCTCACNCGNNANGTTTC 88
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or
                                                             2 AAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTTC
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     canine microarray; drug screening; toxicity assay;
environmental pollutant; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention is related to a novel isolated canine nucleic acid
                     1,
  Pred. No. 6.2e-08;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Novel canine microarray-related DNA sequence SeqID4476.
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                                                                                                                                              84
                                                                                                                                                                                   87 INTICAAACATAAGGAGTAAGAAA 64
                                                                                                                                              61 TCTTCAAACATAAGGAGTTAGAAA
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                                                                                                                                                                                                                                                                                         ADQ53174 standard; DNA; 538
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENE LOGIC INC. (PFIZ ) PFIZER PROD INC.
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Best Local Similarity
Matches 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               living organism.
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                                                                                                                                                                                                                                                                                                                                  ADQ53174;
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of the toxins. The methods are also useful for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the production of a canine microarray of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 ATGNNNNNATACTCAGATAAATTAGTTTCTATTCATTATTTAGATTCCAGATAGGGAGA 476
                                                                                                                                                                                                                                                                                                                                                                                        155 AGTAATTTTCGGAAAAGAAATGATAGCTATATTAAAGCAGATATTCATTACAATACCATG 214
                                                                                                                                                                                                                                                                                                                                                                                                                           475 AACAANNNNNGGCAAAACTATAGATCTATAGAGCAGATGA----CATGACGNNNCCACT 420
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12.0%; Score 54.6; DB 13; Length 538;
Best Local Similarity 55.6%; Pred. No. 3.9e-05;
Matches 135; Conservative 0; Mismatches 99; Indels 9
                                                                                                                                                            Seguence 538 BP; 101 A; 117 C; 110 G; 125 T; 0 U; 85 Other;
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Search completed: May 5, 2005, 00:37:22 Job time : 319.957 secs

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COTHER INFORMATION:
US-08-680-395-8
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Sequence 5519, Ap
Sequence 12147, Ap
Sequence 1731, A
Sequence 1731, A
Sequence 34, Appl
Sequence 34, Appl
Sequence 405, App
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Sequence 34, Appl
Sequence 405, App
Sequence 12386, A
                                                                                                          May 4, 2005, 23:46:20 ; Search time 102.218 Seconds (without alignments) 7283.499 Million cell updates/sec
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Sequence 145869,
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                                                                                                                                                                                                                             1 GAAATCAGAAGTTTAATATG.......ATTGTCCTATTTCNGGGGGT 455
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-12386
US-09-949-016-12386
US-09-949-016-136427
US-08-949-016-136427
US-08-915-972h-1
US-08-915-972h-1
US-09-949-016-13330
US-09-949-016-12552
US-09-949-016-12572
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                                                                                                                                                                                                                                                                                                                            1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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428
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146136, 146137, 146404, 146405,	15851, 15852,		12724,		196367,		12708, 12708, 16723,
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US-09-949-016-146136 US-09-949-016-146137 US-09-949-016-146404 US-09-949-016-146405	US-09-949-016-15851 US-09-949-016-15852	US-09-949-016-15853 US-09-949-016-12387	US-09-949-016-12724 US-09-949-016-12725	US-09-949-016-196365 US-09-949-016-196366	US-09-949-016-196367 US-09-949-016-12896	US-09-949-016-17305	US-09-949-016-1/01/ US-09-949-016-12708 US-09-949-016-16723
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ALIGNMENTS

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US-08-680-395-8

| Sequence | Application US/08680395 |
| SAPIICANT: Collina |
| APPLICANT: Godfrey, Tony |
| APPLICANT: Rowmens, Johanna |
| TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their |
| TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their |
| TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their |
| TITLE OF INVENTION: Genes |
| ADDRESSEE: Townsend and Townsend and Crew Lip |
| STREET: The Embarcadero Center, Eighth Floor |
| CONTRY: California |
| CONPUTER READALE FORM: |
| MEDIUM TYPE: Ripopy disk |
| COMPUTER READALE FORM: |
| MEDIUM TYPE: Ripopy disk |
| COMPUTER READALE FORM: |
| MEDIUM TYPE: Ripopy disk |
| COMPUTER READALE FORM: |
| MEDIUM TYPE: Ripopy disk |
| COMPUTER READALE FORM: |
| MEDIUM TYPE: Ripopy disk |
| COMPUTER READALE FORM: |
| MEDIUM TYPE: |
| APPLICANTON NUMBER: |
| APPLICANTON NUMBER: |
| APPLICANTON NUMBER: |
| SEQUENCE CHARACTERISTICS: |
| TELECOMMUNICATION INTERNATION: |
| RECISTRATION NUMBER: |
| SEQUENCE CHARACTERISTICS: |
| TELEROTH: |
| SEGUENCE CHARACTERISTICS: |
| SEGUENCE C
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; LOCATION: (449)
US-08-892-695-8
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                                                        Gaps
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Sequence 8, Application US/08892695A

Sequence 8, Application US/08892695A

GENERAL INFORMATION:

APPLICANT: Collins, Collin

APPLICANT: Goldins, Collin

APPLICANT: Rowel, David

EARLIER RILING DATE: 1997-01-17

EARLIER FILING DATE: 1997-01-17

EARLIER FILING DATE: 1996-01-16

EARLIER FILING DATE: 1996-07-15

SOFTWARE: PAPPLICATION NUMBER: 08/680, 395

EARLIER FILING DATE: 1996-07-15

SOFTWARE: PAPPLICATION VOWER: 08/680, 395

SOFTWARE: PAPPLICATION VOWER: 08/680, 395
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                       Length 455;
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                                                        0; Indels
                   99.6%; Score 453; DB 2; Le
100.0%; Pred. No. 6.3e-134;
iive 0; Mismatches 0;
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OTHER INFORMATION: n is A,
FEATURE:
NAME/KEY: modified_base
               Query Match
Best Local Similarity 100.
Matches 455; Conservative
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US-08-892-695-8
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Sequence 5619, Application US/09949016

Sequence 5619, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILLE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 00/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PEASESQ for Windows Version 4.0

LENGTH: 4541
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                                                                0; Indels
99.6%; Score 453; DB 4; Le
100.0%; Pred. No. 6.3e-134;
Live 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 455; Conservative
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Best Local Similarity
Matches 450; Conserv
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; ORGANISM: Human
US-09-949-016-5619
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Sequence 17361, Application US/09949016
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, USTORY
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 17361
                                                                                                                                                                                                                                                                                360 CCCACACAGAAATCTGCAGCCCACACAGCTGCCTCCGCCGCTTCCATGTGATCATC 419
765318 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCCTTCCATGTGATCATC 765259
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                                               300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC
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                                                                                                              240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT
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94.1%; Score 428; DB 4; L
Best Local Similarity 99.1%; Pred. No. 3.7e-124;
Matches 450; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                           CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361
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ORGANISM: Human
FEATURE:
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Sequence 12147, Application US/09949016

Sequence 12147, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITLLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPREMENCE: CLOOL 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12147

LENGTH: 176777

WARDENT TO NOTE TO WINDOWS VETSION 4.0
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                                                                                                                                                                                                                                                                                          4302 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGCCTTTGGAGAGTACCATCT 4243
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                                                                                                                                  4421 ATTCATTTCGATTAATTTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 4363
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CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                      ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
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                                                                                            120 ATTCATTTCGATTAATTACCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATA
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94.1%; Score 428; DB 4; L
Best Local Similarity 99.1%; Pred. No. 3.7e-124;
Matches 450; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4122 CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 4089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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US-09-949-016-12147
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US-09-949-016-12147/c
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ORGANISM: Human
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2222 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 2163
                                                                                        2162 ATTCATTTCGATTAATTAAATTCCAGATAGAGAAAGTAATTTT-GGAAAAGAAATGATA 2104
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                                                                                                                                        180 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATATATTTTTGGCA
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: 07-Jun-2001
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/811,481
                                             120 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jelinek, Laura J.
Sheppard, Paul O.
Hagopian, William A.
LaGasse, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS.
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1863 CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: <UNKNOWN>
ATTORNEY AGENT INCORNATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09876527
Patent No. 6627735
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
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SEQUENCE CHARACTERISTICS:
LENGTH: 2328 base pairs
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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765438 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 765379
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                                             300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAAC 359
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                                                                                                                                      360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
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Pred. No. 4.6e-125;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
APPLICANT: Gelinek, Laura J.
APPLICANT: Sheppard, Paul O.
APPLICANT: Hagopian, William A.
APPLICANT: Ladasse, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08811481 Patent No. 6300093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2328 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.78;
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NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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Best Local Similarity 98.9
Matches 449; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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US-08-811-481-34/c
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ORGANISM: Human
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APPLICANT: VENTER, J. Craiq et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                            2222 CTCTTCAAACATAAGGGGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 2163
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                                                                                                                                                                                                                                                                                                                                                           180 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 CCCACACAGGAAATCTGCAGCCCCACACAGCTGCCTCTGCGCCCCTTCCATGTGATCATC 419
                                                                                                                                                                                                                                                                                 120 ATTCATTTCGATTAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                   240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
                                                                                                                                                                                                        CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA
                                                                                                                              1 GAAATCAGAAGTTTAATATGACACAATTAAATATATTGTATATGTCTCACACCGGA-GNTT
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                                                                                           Gaps
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                                                                                           2;
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                                                        DB 4; Length 2328;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 414.6; DB 4;
Pred. No. 3.9e-121;
0; Mismatches 6;
                                                      Score 426.4; DB 4;
Pred. No. 4.6e-125,
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-876-527-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 405, Application US/09949016; Patent No. 6812339
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98.2%;
                                                    Query Match 93.7%;
Best Local Similarity 98.9%;
Matches 449; Conservative (
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Best Local Similarity 98.2
Matches 439; Conservative
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LENGTH: 4719
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pagence 12386, Application US/09949016

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gequence 12386, Application US/09949016

general INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,756

PRIOR PLILNG DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007-012

SOFTWARE: FREESE FORESE OF WINDOWS VERSION 4.0

SEQ ID NO 12386

LENGTH: 263693 251830 251771 AATTATÄTÄTÄÄTTTÄÄTTTÄÄTTTÄTÄTÄTÄTATATTTÄATTTÄATTTAATTTATATT 70 ATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCG ATTAATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATAGCTATAATAA 251951 AATATATTTGATTACATTAAATTATATA 251981

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TYPE: DNA
ORGANISM: Human
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GENERAL METHODS OF DETECTION AND USES THEREOF
GENERAL FILING DATE:
GOOD-40-41
FRIOR APPLICATION NUMBER:
GO/231,768
FRIOR APPLICATION NUMBER:
GO/231,768
FRIOR APPLICATION NUMBER:
GO/231,498
FRIOR FILING DATE:
Z000-10-03
FRIOR FILING DATE:
Z000-09-08
NUMBER OF SEQ ID NOS:
ZOFTWARE:
FRIENCE FREEEQ FOR Windows Version 4.0
SEQ ID NO 35582
LENGTH:
GOFTWARE:
GONTANDER OF SEAUCH
GENERAL GOOD-09
SEQ ID NO 35582
LENGTH:
GONTANDER OF SEQ ID NOS:
GONTANDER GOOD-09
SEQ ID NO 35582
                                                                            GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLILONG DATE: 2000-10-30

PRIOR PLILONG DATE: 2000-10-33

PRIOR FILING DATE: 2000-10-33

PRIOR PLILONG DATE: 2000-10-33

PRIOR PLILONG DATE: 2000-10-33

PRIOR PLILONG DATE: 2000-10-36

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGAGNTTCTCTTCAAAC
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Pred. No. 0.013;
0; Mismatches 104; Indels 0;
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                                           Sequence 16915, Application US/09949016
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Best Local Similarity 50.74
Matches 107; Conservative
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US-09-949-016-35582/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16915
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US-09-949-016-35582
RESULT 10
US-09-949-016-16915
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DETECTION AND USES THEREOF
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APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Wincent Brichard
TITLE OF INVENTION: MHICH FORM COMPLEXES WITH MHC MOLECULE HLA-A2
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 136427, Application US/09949016
; Sequence 136427, Application US/09949016
; Patent No. 681239
; GREERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AN FILE REPERENCE: CL001307, CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; RIGHARD APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136427
Query Match 9.5%; Score 43; DB 4; Length 601; Best Local Similarity 56.4%; Pred. No. 0.0021; Matches 79; Conservative 0; Mismatches 61; Indels
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56.4%; Pred. No. 0.0021;
tive 0; Mismatches 61; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AGATAGAGAGAAGTAATTTT 163
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Matches 79; Conserv
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US/08/915,972A

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APPLICATION NUMBER:
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TOPOLOGY:
US-08-915-972A-1
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APPLICANT: Yannick Guilloux; Francine Jotereau;
APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Vincent Brichard
APPLICANT: Vincent Brichard
TITLE OF INVENTION: COMPLEXES WITH MHC MOLECULE HLA-A2 AND USES THEREOF UNDER OF SEQUENCES: 21
CORRESPONDENCES. ADDRESS:
ADDRESSE: Fulbright & Jaworski
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 CAATTAAATATATTTGTATATCTCACACCGGAGNTTCTTCTAAACATAAGGAGTTAGAA
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Pred. No. 0.0045;
0; Mismatches 61; Indels
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                                                                                                                                   E: 3.5 inch 1.44 Mb storage diskette
IBM PS/2
                                                                                                                                                                             CURRENT ADDRESS PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/487,135B
FILING DATE: 07-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION ATA:
APPLICATION MABER: 08/487,135
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5821122man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5388
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 110 NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1508 AAGÍCCATÁGTACTAÁTÍTÍ 1527
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Best Local Similarity 56.4%;
Matches 79; Conservative
805 Third Avenue
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STRANDEDNESS: single
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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US-08-487-135B-1
                   New York
New York
Y: USA
                                                                                                                                                                 COMPUTER:
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                                                                   COUNTRY:
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TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES PEPTIDES WHICH
TITLE OF INVENTION: FORM COMPLEXES WITH MHC MOLECULE HLA-A2 AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pulbright & Jaworski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1388 СААТТТТАТGТАТТТGAATATCAGCAAATTGAAATTTTCCATAATTATCATTAATTTGTA 1447
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0
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MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yannick Guilloux; Francine Jotereau;
APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Vincent Frichard
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL T
                                                                                                                                    NAME: Hanson, No. 5886145man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5388 - JEL/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 639-3894
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,909
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805 Third Avenue
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,135
FILLING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: August 21, 1997
APPLICATION NUMBER: 08/487,135
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5958711man D
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; Sequence 1, Application US/09177909
; Patent No. 5958711
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REGISTRATION NUMBER: 30,946
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: USA
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Search completed: May 5, 2005, 07:03:25 Job time: 110.552 secs

1508 AAGTCCATAGTACTAATTT 1527

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3.5
43.2
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1: /cgn2_6/ptodate/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodate/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodate/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodate/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodate/2/pubpna/US06_NEW_PUB.seq:*
6: /cgn2_6/ptodate/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodate/2/pubpna/US08_NEW_PUB.seq:*
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13: /cgn2_6/ptodate/2/pubpna/US09E_PUBCOMB.seq:*
13: /cgn2_6/ptodate/2/pubpna/US09E_PUBCOMB.seq:*
14: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
17: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
18: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
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todata/2/pubpna/US10F_PUBCOMB.seq:
                                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5654200 segs, 3057283753 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 8, Appli	Sequence 1845, Ap	Sequence 34, Appl	Sequence 34, Appl	Sequence 435, App	Sequence 1301, Ap	Sequence 2332, Ap	Sequence 93, Appl	Sequence 192, App	Sequence 18, Appl	Sequence 27, Appl
QI.	US-08-731-499-8	US-10-106-698-1845	US-09-876-527-34	US-10-124-089-34	US-10-887-553A-435	US-10-060-036-1301	US-10-106-698-2332	US-10-240-485-93	US-10-311-455-192	US-10-257-166-18	US-10-433-793-27
DB	6	15	o	16	19	14	15	15	15	17	18
Length	455	1258	2328	2328	4767	282	455	6811	11422	11422	37515
* Query e Match Length DB]	99.6	96.5	93.7	93.7	93.6	56.0	14.2	9.7	9.7	9.7	9.7
Score	453	439	426.4	426.4	426	254.8	64.4	44.2	44.2	44.2	44.2
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Sequence 180643, Sequence 217, App Sequence 217, App Sequence 217, App Sequence 11, Applia Sequence 126, App Sequence 244, Appl Sequence 29543, A Sequence 29543, A Sequence 29544, A Sequence 175, App Sequence 175, App Sequence 175, App Sequence 175, App Sequence 157, App Sequence 1577, App Sequence 1577, App Sequence 1571, App Sequence	Sequence 14
US-10-027-632-180643 US-09-252-298-217 US-09-252-298-217 US-10-1028-217 US-10-1028-217 US-10-1028-1144-513 US-10-312-841-1 US-10-312-841-1 US-10-311-455-1290 US-10-311-455-12414 US-10-311-455-12414 US-10-312-841-2 US-10-313-841-2 US-10-313-841-2 US-10-313-841-2 US-10-313-85-2943 US-10-313-85-2944 US-10-313-85-136 US-10-21-1455-176 US-10-21-1448-260 US-10-21-1448-260 US-10-21-1448-260 US-10-21-1448-157 US-10-21-1448-157 US-10-33-3458-1577 US-10-33-3458-1577 US-10-33-3458-1577 US-10-33-3458-1577 US-10-33-3458-1577 US-10-33-4838-1578 US-10-38-128-1178 US-10-28-1228-11278	10-311-455-144 LIGNMENTS end and Crew r, 8th Floor 0S 0, Version #1 499
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                 Length 1258;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
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NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: ZymcGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                               Score 439; DB 15;
Pred. No. 2.5e-103;
0; Mismatches 2;
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                                                                                                                                                          ; LOCATION: (1237)...(1237); OTHER INPORMATION: n equals a,t,g, or uUS-10-106-698-1845
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Sheppard, Paul O.
Hagopian, William A.
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Patent No. US20020102616A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               Query Match 96.5%;
Best Local Similarity 99.3%;
Matches 450; Conservative
                    SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 1845
LENGTH: 1258
NUMBER OF SEQ ID NOS: 8564
                                                                                  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                     NAME/KEY: misc_feature
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR PELICATION NUMBER: US/100/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1995-09-29
PRIOR FILING DATE: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAA 120
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Pred. No. 3.7e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Pred. No. J.
0; Mismatches
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           REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 2307/
TELECOMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..455
OTHER INFORMATION:
OTHER INFORMATION:
  Hunter, Tom
                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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US-10-106-698-1845/c
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1863 cricircaardaacreaarrerccrarrercege 1830
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                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,089
FILING DATE: 16-Apr-2002
CLASSIFICATION: cUnknown.
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/811,481
FILING DATE: cUnknown.
ATORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
REFERENCE/DOCKET NUMBER: 95-36
                                           ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6675
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2328 base pairs
                                                                                                                                            ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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    NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 449; Conservative
                                                                                   CITY: Seattle STATE: WA
                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-124-089-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2043 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1983 ATCTAAGATGGAGGAATGCTGTGGGAAGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2282 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTTGTATATCTCACACCGGAGGTTT 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2222 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1923 CCCACACAGGAAATCTGCAGCCCACGCAGCTGCCTCTGCGCCCCTTCCATGTGATCATC 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2162 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCATTTCGATTAATTTAAATTCCAGATAGAGAAGGTAATTTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 ATCTAAGATGGAGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCTTCCATGTGATCATC 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.7%; Score 426.4; DB 9;
98.9%; Pred. No. 5.9e-100;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1863 cregricalidadergaarrerccraftrereege 1830
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Sheppard, Paul O.
Hagopian, William A.
LaGasse, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: 07-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 95-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/811,481
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/10124089
Publication No. US20030166067A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            TELEFAX: 206-442-6678
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2328 base pairs
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                                                                                                                                 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.9
Matches 449; Conservative
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2222 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 2163 2162 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAATTTT-GGAAAAGAAATGATA 2104 1923 cccacacacacaaaarcrocacccacccaccaccrocrocccccccroccarcracarcarc 60 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 120 ATTCATTTCGATTAATTAAATTCCAGATAGAGAAGGAAGTAATTTTCGGAAAAGAAATGATA 2103 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAAGCAATATTTGGCA 2043 rearrererececreagrasseceirerrecereresarassecerringassasasarer ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAAC CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC 1 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTT 2282 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATTTCTCACACCGGAGGTTT GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT Gaps Score 426.4; DB 16; Length 2328; Pred. No. 5.9e-100; 0; Mismatches 3; Indels 2; COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0

2044

179

1984

419

2223

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Query Match
Best Local Similarity 98.2
Matches 278; Conservative
                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-060-036-1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4579 TATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCATC 4520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4519 ATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCTAT 4460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4459 CTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAACCC 4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CITCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 TCATITCGATTAATTAAATTCCAGATAGAGAAGAAGTAATTTTCGGAAAAGAAATGATAGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TATATTAAAGCAGATATTCATTACAATACCATGTAGAGCATAAGCAATATTTTGGCATC 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4767;
                               Sequence 435, Application US/10887553A
| Publication No. US20050085436A1
| GENERAL INFORMATION:
| APPLICANT: Li, Hao
| TITLE OF INVENTION: With insulin signalling dysregulation
| TITLE OF INVENTION: With insulin signalling dysregulation
| FILE REFERENCE: 4-33262 |
| CURRENT APPLICATION NUMBER: US/10/887,553A |
| CURRENT FILING DATE: 2004-07-08 |
| PRIOR FILING DATE: 2003-08-07 |
| NUMBER OF SEQ ID NOS: 1208 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 435 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-060-036-1301/C
US-10-060-036-1301, Application US/10060036
; Sequence 1301, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Ralos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 426; DB 19; Length 4
Pred. No. 1e-99;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCAATGAAGTGAATTGTCCTATTTCNGGGG 453
                                                                                                                                                                                                                                                                                                                                                                                                                          93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 93.6
Best Local Similarity 99.1
Matches 448; Conservative
RESULT 5
US-10-887-553A-435/c
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                      US-10-887-553A-435
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US-10-106 698-2332/C

Sequence 2332, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTURO: Colon and Colon Cancer Associated Polynucleotides and Polypeptides:

TILE REFERENCE: PAONOFP1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280

SPIOR APPLICATION NUMBER: US 60/163,280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 ATAAGTAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GTTTAATATGACACAATTAAATATTTTTGTATATCTCACACCGGAGGTTTCTCTTCAAAC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.0%; Score 254.8; DB 14; Length 98.2%; Pred. No. 6.7e-56; ive 0; Mismatches 3; Indels
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TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
                    FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (8)...(8)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: (86)...(86)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (83)...(85)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (93)...(93)...(93)...(93)...(93)...(93)...(93)...(93)...(93)...(93)...(93)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)...(94)
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LCGATION: (95).
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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us-08-731-499-8.rnpb

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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-485-93
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REPREENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT PILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-09-01
                                                                                                      CCCATION: (1267..(126)

OTHER INFORMATION: n equals a, t, g, or c
MAMB/KEX: mist C feature
LOCATION: (148)...(148)

OTHER INFORMATION: n equals a, t, g, or c
LOCATION: (180)...(180)

OTHER INFORMATION: n equals a, t, g, or c
LOCATION: (1257...(225)

OTHER INFORMATION: n equals a, t, g, or c
LOCATION: (2257...(225)

OTHER INFORMATION: n equals a, t, g, or c
LOCATION: (375)...(375)

OTHER INFORMATION: n equals a, t, g, or c
NAME/KEX: mist C feature
LOCATION: (377)...(375)

OTHER INFORMATION: n equals a, t, g, or c
NAME/KEX: mist C feature
LOCATION: (387)...(387)

OTHER INFORMATION: n equals a, t, g, or c
NAME/KEX: mist C feature
LOCATION: (387)...(425)

OTHER INFORMATION: n equals a, t, g, or c
NAME/KEX: mist C feature
LOCATION: (425)...(425)

OTHER INFORMATION: n equals a, t, g, or c
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COCATION: (438)...(438)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (454)...(454)
OTHER INFORMATION: n equals a,t,g, or c
VICEN INFORMATION: n equals a,t,g, or c
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             LOCATION: (99)..(99)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Artificial Sequence
FEATURE:
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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NOS: 2424
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                                                                                                                                                                                                                                          71 TAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAAATTCATTTCGA
                                                                                                                                                                                                                                                                                                    131 TTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATGATATTTAAA
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                                                                Gaps
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-192
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Score 44.2; DB 15; Length 6811;
Pred. No. 1;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 192, Application US/10311455
Publication No. US20030143606A1
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ORGANISM: Artificial Sequence
   Query Match
Best Local Similarity 51.5%;
Matches 100; Conservative
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191 GCAGATATTCATTA 204

131 TTAATTAAATTCCAGATAGAGAGAAGTAATTTTCGGAAAAGAAATGATAGCTATATTAAA

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                        Sequence 18, Application US/10257166
Fublication No. US20040022330A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DEFENDROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
CURRENT APPLICANTION NUMBER: US/10/257,166
CURRENT PILING DATE: 2002-10-07
FRIOR APPLICATION NUMBER: PCT/EP01/07470
BE 10032529.7
BE 10033529.7
FRIOR FILING DATE: 2001-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/10433793
Publication No. US20040142334A1
GENERAL INFORMATION:
APPLICANT: Epidenomics AG
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
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Pred. No. 2.2;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-433-793-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-257-166-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.2; DB 17; Length 11422;
Pred. No. 1.3;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%;
Best Local Similarity 51.5%;
Matches 100; Conservative 0
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Best Local Similarity 51.5%;
Matches 100; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 178
SEQ ID NO 18
LENGTH: 11422
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Best Local Similarity
                      -10-257-166-18/c
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LENGTH: 37515
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US-10-433-793-27
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283 AAGAGGAGAGTGGAACATTTCAAATTATTGGAAAAAATCAAGCTGGAATTGAATATCCAA 342
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Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

PRIOR FILING DATE: 2000-07-20

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR PRIING DATE: 1999-09-08

PRIOR PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PRINGS PRICE 1999-108-08

PRIOR PRINGS PRICE 1999-108-08
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Pred. No. 0.66;
0; Mismatches 109;
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6548 AACGAGGTTTATTA 6561
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Best Local Similarity 49.8<sup>†</sup>
Matches 108; Conservative
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US-10-027-632-180643
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ORGANISM: Human
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11 GTTTAATATGACACAATTAAATATTTGTATATCTCACACCGGAGNTTCTCTTCAAACA 70

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RESULT 15
US-10-102-806-217
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                                        JUNEARL INFORMATION:
JUNEARLY: Wang, David G.
JITLE OF INVENTION: Identification and Mapping of Single Nucleotide
JITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-34
PRIOR PILING DATE: 2000-02-34
PRIOR PILING DATE: 2000-02-34
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO3

CURRENT APPLICATION NUMBER: US/09/925,298

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/USO0/05881

PRIOR APPLICATION NUMBER: PCT/USO0/05881

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: PATENTI Ver. 2.0

SEQ ID NO 217

LENGTH: 2815
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Best Local Similarity 49.8%; Pred. No. 0.66;
Matches 108; Conservative 0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 217, Application US/09925298 Publication No. US20020039764A1
Publication No. US20030204075A9
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-925-298-217
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; ORGANISM: Human
US-10-027-632-180643
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LENGTH: 670
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                                                         Gaps
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GENERAL INCOMPATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO3PLC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR SEC ID NOTE: 1999-03-12

NUMBER OF SEC ID NOTE: 1999-03-12

SEC ID NO 217

LENGTH: 2815
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Length 2815;
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Query Match
9.5%; Score 43; DB 9;
Best Local Similarity 56.4%; Pred. No. 1.4;
Matches 79; Conservative 0; Mismatches 6
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Job time : 635.302 secs
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                                                                                                                                                                                                                                                                                                                                                                                2077 AACTCCATAGTACTAATTTT 2096
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Matches 79; Conservative
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; ORGANISM: Homo sapiens
US-10-102-806-217
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	encore version :	- 2005 (
C	Gencore	(c) 1993
		Copyright

OM nucleic - nucleic search, using sw model

May 4, 2005, 23:17:50 ; Search time 1925.91 Seconds (without alignments) 8992.766 Million cell updates/sec Run on:

US-08-731-499-8 455 1 GAAATCAGAAGTTTAATATG......ATTGTCČTATTTCNGGGGGT 455 Title: Perfect score: Sequence:

Scoring table:

34239544 seqs, 19032134700 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

68479088

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST: * Database :

9b est1: 9b est2: ; ; 9b htc: ; ; 9b est4: ; ; 9b est6: ; ; 9b gss1: ; 9b gss2: ; ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	at		N78571	BI712448	AA661732	AI082095	BE044633	BU728730	AI955290	BU069389	AI828084	BQ019198	BM985176	HSM802434	BM272161	CA775968	AI433898	BM353165	BQ778146	AI425012	BU077543	CK822118	CB850986	BX104775	AA563807	AA460668
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	* Query Match Length DB	1000	455	458	471	472	478	530	539	557	563	642	715	2413	454	499	459	461	486	519	561	586	782	551	449	447
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			AI276830 q167£01.x		BQ787950 il45e02.x	AL572501 AL572501		BG059906 naf45f08.	AI082653 0x59a02.8	AI148116 qb43e06.x		AA101715 zk95h12.s	AW662836 hi82c03.x	AI378227 tc65c09.x	AI148121 qb43e12.x	-	CR590102 full-leng	AL573342 AL573342	CR596761 full-leng	AI972872 wr44£07.x
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91	5	16	91.2	9	90	90	89.6	83	89	88	88	88	87	87	87	87	87	86	85	82
416	416	415.2	415	413	410.6	410.6	407.6	406.4	405	404	402.6	402.2	398	398	398	396.8	395.8	391.6	389.8	388
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ALIGNMENTS

455 b etal_lung_N NA sequence 2	i Chordata; Catarrata; Vertebrata; Primates; Catarrhini; Hominidas; N., Dubuque, T., Elliston, K., Hawki, M., Kucaba, T., Le, M., Lennon, G., L., Rohlfing, T., Soares, M., Tan, Eston, R., Williamson, A., Wohldmanr Project	Contact: Wilson RK Contact: Wilson RK 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1800 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: ml3 -40 forward High quality sequence stop: 390.	1. 455 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GBE:1245017" /db_xref="GBE:1245017" /db_xref="cdBE:1245017" /db_bost="bmade:300093" /clone="lbase="19" weeks" /lab_host="DH10B (ampicillin resistant)" /clone lib="Soares fetal lung NbH119W" /note="Organ: lung, Vector: pT7T3D (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGGGGGGGGGGGGGCAATTTTTTTTT
RESULT 1 N78571 LOCUS DOFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	COMMENT	BOULCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 CCCACACAGGAAATCTGCAGCCCCACAGCTGCCTCTGCGCCCCTTCCATGTGATCATC 422
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAAGTAATTTT-GGAAAAGAAATGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAAGCAATATTTTGGCA
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Pred. No. 7.6e-104;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="teaxon:9606"
/db_xref="IMAGE:5086349"
/tissue_type="Purified pancreatic islet"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
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Seg primer: -40UP from Gibco
High quality sequence stop: 446.
Location/Qualifiers
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(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 458)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Helienishka, I., Scaerce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Gardens, M., Gibbons, M., Gronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium
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                                                                                                                                                                                                                          99.6%; Score 453; DB 7; Length 455; 100.0%; Pred. No. 1.5e-110; ive 0; Mismatches 0; Indels
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Email: dmelton@biohp.harvard.edu
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KEYWORDS
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7

Gaps 2; 119

63

179 182 239 242 299 362 419

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/lab host="DH10B"
/clone lib="Soares NhHMPu S1"
/clone libe made libe modified polylinker; Site l: Not I;
Site 2: Eco R1; Equal amounts of plasmid DNA_from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHHPU, and fetal heart NbHHPM) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
                                                                                                                                                AI082095 472 bp mRNA linear EST 01-OCT-1998 o238a05.81 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677584
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/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.mih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 562 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 464.
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99.1%; Pred. No. 7.6e-104;
iive 0; Mismatches 2;
      420 CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 453
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/db_xref="taxon:9606"
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Homo sapiens
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                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llhl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="normal prostate"
/lab_host="DH10B"
/clone_lib="NGI_GGAP_Pr22"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 471). NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.cbi.natitute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1219187"
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/organism="Homo sapiens"

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/db_tref="txxxon:9606"

/clone="type="human retina"

/dev_stage="dath"

/dev_stage="dath"

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/dev_stage="nBH208" (Life Technologies) (T3 phage resistant)"

/dev_stage="nBH208" (Life Technologies) (T3 ite 2: Not I;

/dev_stage="nBH208" (Life Technologies) (T3 ite Cancaring the following tissue(8): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Pirst strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double
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I (basea 1 to 530)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                    193 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA
                                                                                                                                                                                                     253 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCCTTTGGAGGTACCATCT
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UI-E-CL1-aep-b-05-0-UI 3', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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Email: cgapbs-romail.nih.gov
Tissue Procurement: Klaus Kaserer, M.D., Chris Moskaluk, M.D.,
Tissue Procurement: Klaus Kaserer, M.D., Chris Moskaluk, M.D.,
Ph.D., Michael R. Emmert-Buck, M.D., P.hD.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@lange.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 bp mRNA linear EST 08-JUN-2000 hg87e04.x1 NCI_CGAP_Thy3 Homo sapiens cDNA clone IMAGE:3126366 3', mRNA sequence.
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/db_xref="taxon:9606"
/clone="ImAds:116366"
/tissue_type="follicular carcinoma"
/tab_bogs="Dilog CaAP Thy3"
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/note="Organ: thyroid; Vector: pCMV-SPORT6; Site_1: Not1; Stre_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.4 kb. Library constructed by Life Technologies. "
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   ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
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NCI-CAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                         363 CCCACACAGAGAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC
                                                                                                                                             CCCACACAGGAAATCTGCAGCCCACAGCTGCTCTGCGCCGCCTTCCATGTGATCATC
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29 63 119 123 179 182 239 242 299 302 359 362 419 422

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1m21205.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6035601
37, mRNA sequence.
                                                                                                                                                               1. .539

Corganism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="INAGE:2545354"

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/clone lib="NCI_Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies."
                   Clone distribution: NCI-CGAP clone distribution information can distribution information can disturbed the I.M.A.G.B. Consortium/LLNL at:
www.blo.llnl.gov/bbrp/lmage/image.html
Insert Length: 2000 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 414.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 557)
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
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0; Mismatches 2;
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al Similarity 99.1%;
450; Conservative (
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                 with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of lists-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI).

TAG_LIB=UI.E-CCGCC.
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wx32c06.xl NCI CGAP_Pitl Homo sapiens cDNA clone IMAGE:2545354 3',
mRNA sequence.
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(Dases 1 to 539)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
stranded cDNA was ligated to an EcoR I adaptor, digested
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies,
Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
Consortium DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                   19 GAAATCAGAAGTTTAATATGACACAATTAAATATATTGTATATATCTCACACCGGAGGTTT
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                                                                                                                                                                                                                                                                        Score 428; DB 5; L
Pred. No. 7.8e-104;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                     94.1%;
Local Similarity 99.1%;
les 450; Conservative (
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мк31f02.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413947 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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/lab_host="DH108"
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Seq

Clone distribution: NCL-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1234 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 482.

Location/Qualifiers
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larity 99.1%; Pred. No. 7.9e-104;
Conservative 0; Mismatches 2;
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                                                           436 CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 469
                               420 CTGGTCAATGAAGTGAATTGTCCTATTTCNGGGG
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                  AI828084.1 GI:5448755
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Xho1; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please conteat Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
aboratory, Washington University School of Medicine, Box
B127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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                                                                                                                                                                                            Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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                                                                                                                                                                                                                                                                                                      rel: 617-495-1812
Fax: 617-495-8512
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
Diversity Geneme Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
seq primer: -40UP from Gibco
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenes, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
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                                                                                                                                         Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
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/db_xref="taxon:9606"
/clone="IMAGE:6035601"
/tissue_type="insulinoma"
/lab_host="PH10B (phage-resistant)"
/clone_lib="Human insulinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .557
/organism="Homo sapiens"
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Location/Qualifiers
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site and the (dT)18 tail. The sequence tag for library is AACTGTTCGG. TAG TISSUE-lung metatastic chondrosarcoma TAG_SEQ=AACTGTTCGG"
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                                                                                                                                                  Score 428; DB 5;
Pred. No. 8e-104;
0; Mismatches 2
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Best Local Similarity 99.1%;
Matches 450; Conservative
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UI-H-DTL-awn-i-24-0-UI.81 NCI CGAP_DT1 Homo sapiens cDNA clone
BQ019198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an olign-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecos I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LiML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
POUYA-YES.
                                                                       241
                                                                                                               299
                                                                                                                                                                                              300 ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
                                                                                                                                                                                                                 360 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCGCCTTCCATGTGATCATC 419
                                                                                                                                                                                                                                                                                                     362 CCCACACAGGAAATCTGCAGCCCACACAGCTGCCTCTGCGCCCCCTTCCATGTGATCATC 421
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/note="Organ: Lung; Vector: pT713.Pac (Pharmacia) with a modified polylinks: Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DTI is a normalized cDNA library containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 642) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                      GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTGGCA
                                                                                                               TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Metastatic Chondrosarcoma"
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 455
                                                                                                                                                                                                                                                                                                                                                           CIGGICAAIGAAGIGAAIIGICCIAIIICNGGGG 453
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'organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5891807"
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EST.
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Unpublished (1997)
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UI-CF-EC1-acc-k-02-0-UI.81 UI-CF-EC1 Homo sapiens cDNA clone
BM985176
                                                                                                                                                                                                                                     120 ATTCATTTCGATTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                180 GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA 239
                                                                                                                                                                                                                                                                                                                                                          240 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                   84 CTCTTCADACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGAGGTGCGTTTTCTACGCTGAAC 359
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Normalization and subtraction: two approaches to facilitate gene
                                                                         24 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATATCTCACACCGGAGGTTT
                                              1 GABATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTT
Gaps
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Thu May

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2413 bp mRNA linear HTC 22-SEP-2004
Homo sapiens mRNA; CDNA DKFZp761A0712 (from clone DKFZp761A0712).
ALIS7451
ALIS7451.1 GI:7018465
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/tb xref="Uniprot/TreMBL:09NSR5"
/translation="VPKNRSLAVLTYDHSRVLLKAENSHSBYINASPIMDHDPRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYIATGGFLPATVADFWQMVWESGCVVIVMLTPLAENGVRQCYHYWFDEGSNLYHIYE
VNLVSEHIWCEDFLVRSFYLKOLQTNETRTVTQFHFLSWYDRGVPSSSRSLLDFRRKV
NKCYRGRSCPIIVHCSDGAGRSGTYVLIDMVLNKWAKGAKEIDIAATLEHLRDQRPGM
VQTKRQFEFALTAVABEVNALLKALPQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 CTCTTCAAACATAAGGAGTTAGAAATTACAAGTAGGCATATGCTTCCTATATTCAGATAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Genome Project.

This clone (DKF2p761A0712) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomicorschung GmbH in Berlin, Germany.
Please conteat RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761A0712
Further information about the clone and the sequencing project is
available at http://mips.ggf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="DKFZp761A0712"
/tissue type="amygdala"
/clone lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites Not1 + Sal1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAATCAGAAGTTTAATATGACACAATTAAATATATTTGTATATCTCACACCGGA-GNTT
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Submitted (22-SEP-2004) MIPS, Ingolŝtaedter Landstr.1, D-85764
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor type,
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99.1%; Pred. No. 1e-103;
ive 0; Mismatches 2; Indels
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/note="protein tyrosine phosphatase,
polypeptide 2, N-terminus truncated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="RZPD:DKFZp761A0712"
/db_xref="taxon:9606"
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/gene="DKFZp761A0712"
/codon_start=1
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Matches 450; Conservative
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                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Lung" | Colored |
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/dev stage="Adult and Fetal" |
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/doo_lib="Ul-CF-EC1" |
/doo_lib="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site=1: BooR i; Site=2: Not I;
/ul-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Jennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr prime containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the Name of the synthesis and the synthesis was prime the synthesis to first-strand cDNA contains a library tag sequence that is located between the Not I site and the synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTCATTTCGATTAATTTAAATTCCAGATAGAGAAGTAATTTTCGGAAAAGAAATGATA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAAGCAATATTTTGGCA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 299
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DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
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llarity 99.1%; Pred. No. 8.2e-104;
Conservative 0; Mismatches 2;
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                                                                             2158 TCATTCTGTCCGCTCAGTAGGCCGTGTTCCCTCTGGTAGGGCCTTTGGAGAGTACCATCT 2099
2277 ATTCATTTCGATTAATTAAATTCCAGATAGAGAGAAGTAATTTT-GGAAAAGAAATGATA 2219
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Email: dmeltonebiohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
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Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                         GCTATATTAAAGCAGATATTCATTACAATACCATGTAGAGACATAAGCAATATTTTGGCA
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ig39h05.x1 HR85 islet Homo sapiens CDNA 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 454)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
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| Da_xref="taxon:9606"
| Cissue_type="Purified pancreatic islet"
| lab_host="DH10B"
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High quality sequence stop: 447.
Location/Qualifiers
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Seq primer: -40UP from Gibco
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CA775968 499 bp mRNA linear EST 03-DEC-2002 ip01h07.xl HR85 islet Homo sapiens cDNA clone IMAGE:6134653 3',
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1 (bases 1 to 499)
Mahton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Endocrine Pancreas Consortium

Upublished (2000)
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
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                                                                                                                                                                                                                                                                                                                       9
School of Medicine, Box 8127, 660 South Euclid Ave., St
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                              Length 454;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                              93.8%; Score 427; DB 4; I
larity 99.1%; Pred. No. 1.4e-103;
Conservative 0; Mismatches 2;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCI CGAP Kidl1"
/clone lib="NCI CGAP Kidl1"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and Fatima Bonaldo. "Batima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTAAGATGGAGGAATGCTGTGGGAAGGGCGGGATGGGAGGTGCGTTTTCTACGCTGAAC 361
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                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 5.5e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 CTGGTCAATGAAGTGAATTGTCCTATTTCTGGGG 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                         Seg primer: -40UP from Gibco
High quality sequence stop: 452
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2130788"
/lab_host="DH108"
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                                                               Tumor Gene Index
Unpublished (1997)
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REFERENCE
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                                                                                                                                                                                                                                                                                         /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site 2: Xho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~lkb. 5;
Xho1 site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI433898 459 pp mRNA linear EST 30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 499;
obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                               /organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="caxon:0606"
/clone="IMAGE:6134653"
/rissue Yrpe="Purified pancreatic islet"
/lab host="Dun108"
/clone_lib="HR85 islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 426.4; DB 6;
Pred. No. 2.1e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                     (hinoue@im.wustl.edu)
Seg primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
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98.9%;
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AI433898
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SOURCE
ORGANISM
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AI433898
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Search completed: May 5, 2005, 06:54:12 Job time : 1935.24 secs

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